

PEPTIDE-LINKER- β CHAIN CONSTRUCT

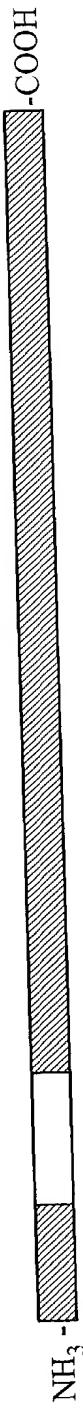


FIG. 1A

SCHEMATIC VIEW OF PEPTIDE-LINKED MHC BINDING GROOVE

β_1 -aa:1

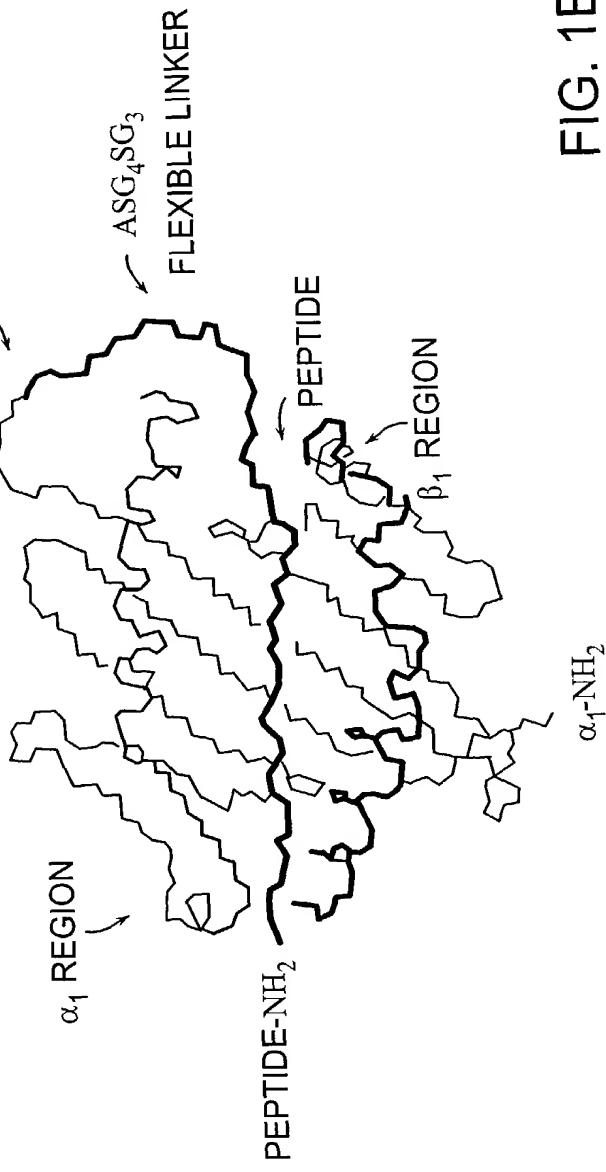


FIG. 1B

SCHEMATIC VIEW OF SOLUBLE PEPTIDE-LINKED MHC-IgG C-REGION FUSION PROTEIN

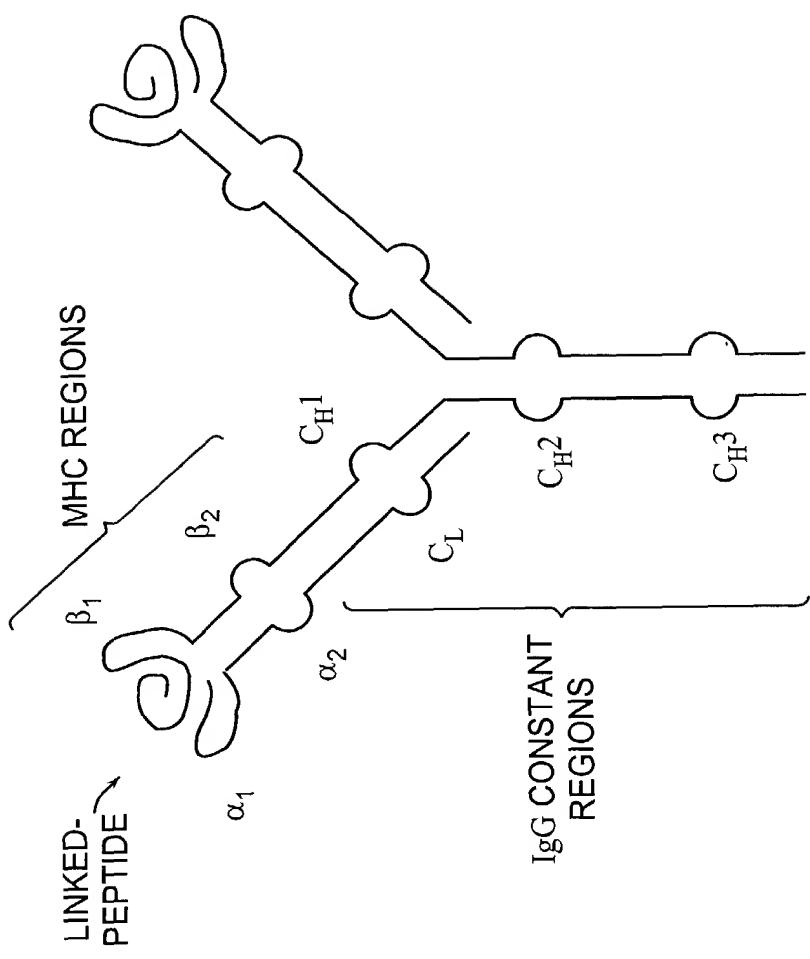


FIG. 1C

Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

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I-A^d α CHAIN CLONING SCHEME

TOTAL RNA ISOLATED
FROM A20 CELLS

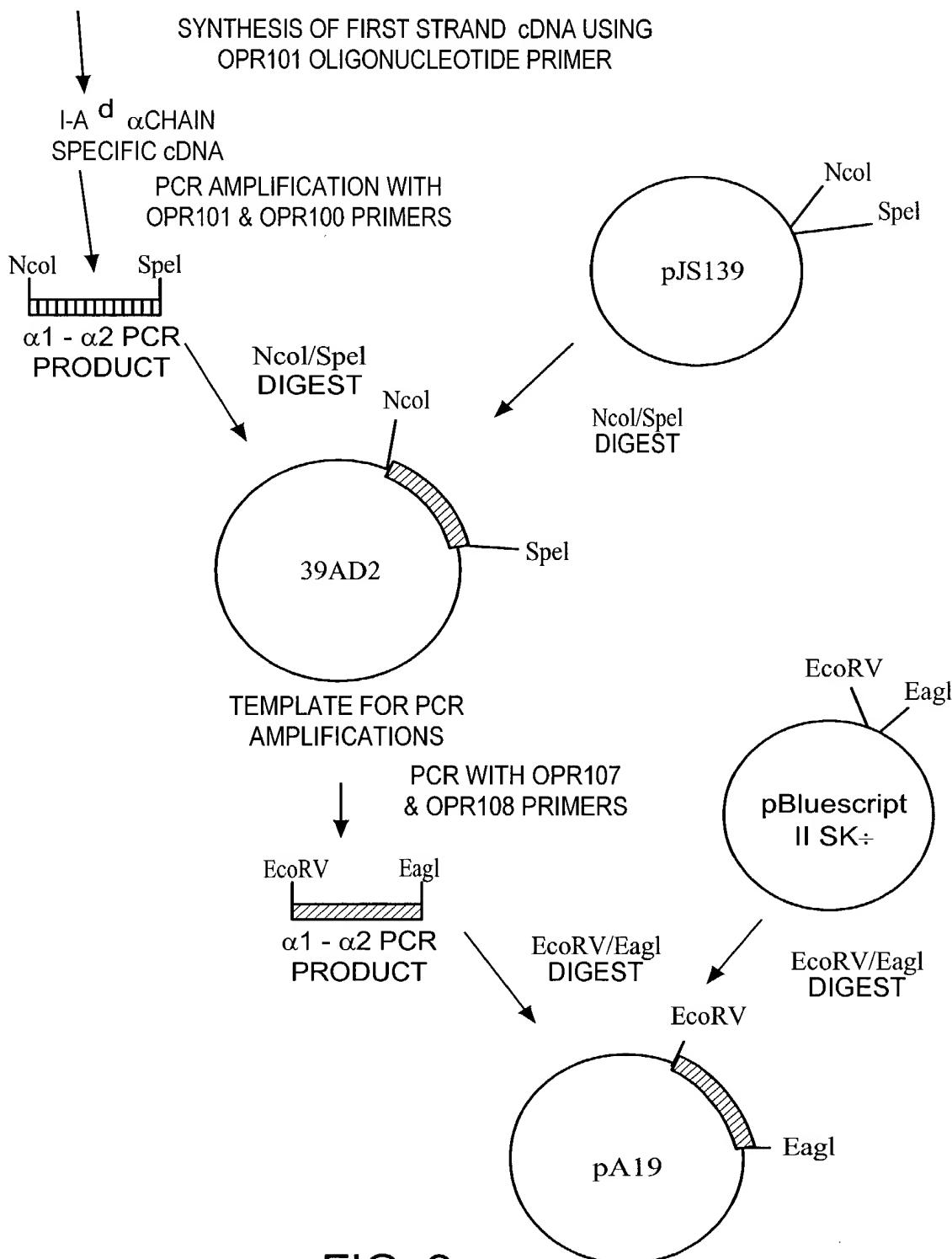


FIG. 2

I-A^d β CHAIN CLONING SCHEME

TOTAL RNA ISOLATED
FROM A20 CELLS

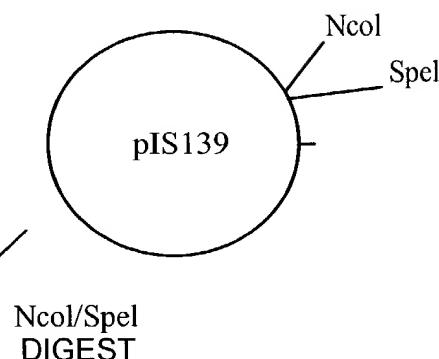
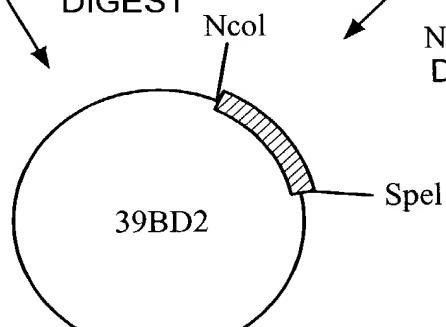
SYNTHESIS OF FIRST STRAND cDNA USING
OLIGO dT PRIMER

cDNA TEMPLATE

PCR AMPLIFICATION WITH
OPR102 & OPR104 PRIMERS

Ncol Spel
β1 - β2 PCR
PRODUCT

Ncol/Spel
DIGEST

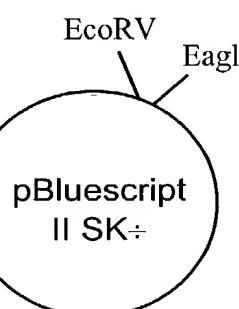


TEMPLATE FOR PCR
AMPLIFICATIONS

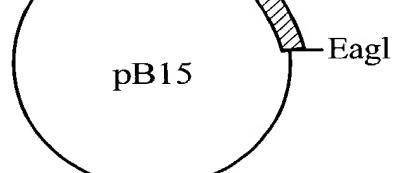
PCR WITH OPR106
& OPR112 PRIMERS

EcoRV Eagl
NheI
AflII
LINKER-β1-β2
PCR PRODUCT

EcoRV/Eagl
DIGEST



HindIII AflII
NheI



MUTATION IN LINKER REGION-
NO EcoRV SITE PRESENT

FIG. 3A

FIG. 3B

FIG. 3

FIG. 3A

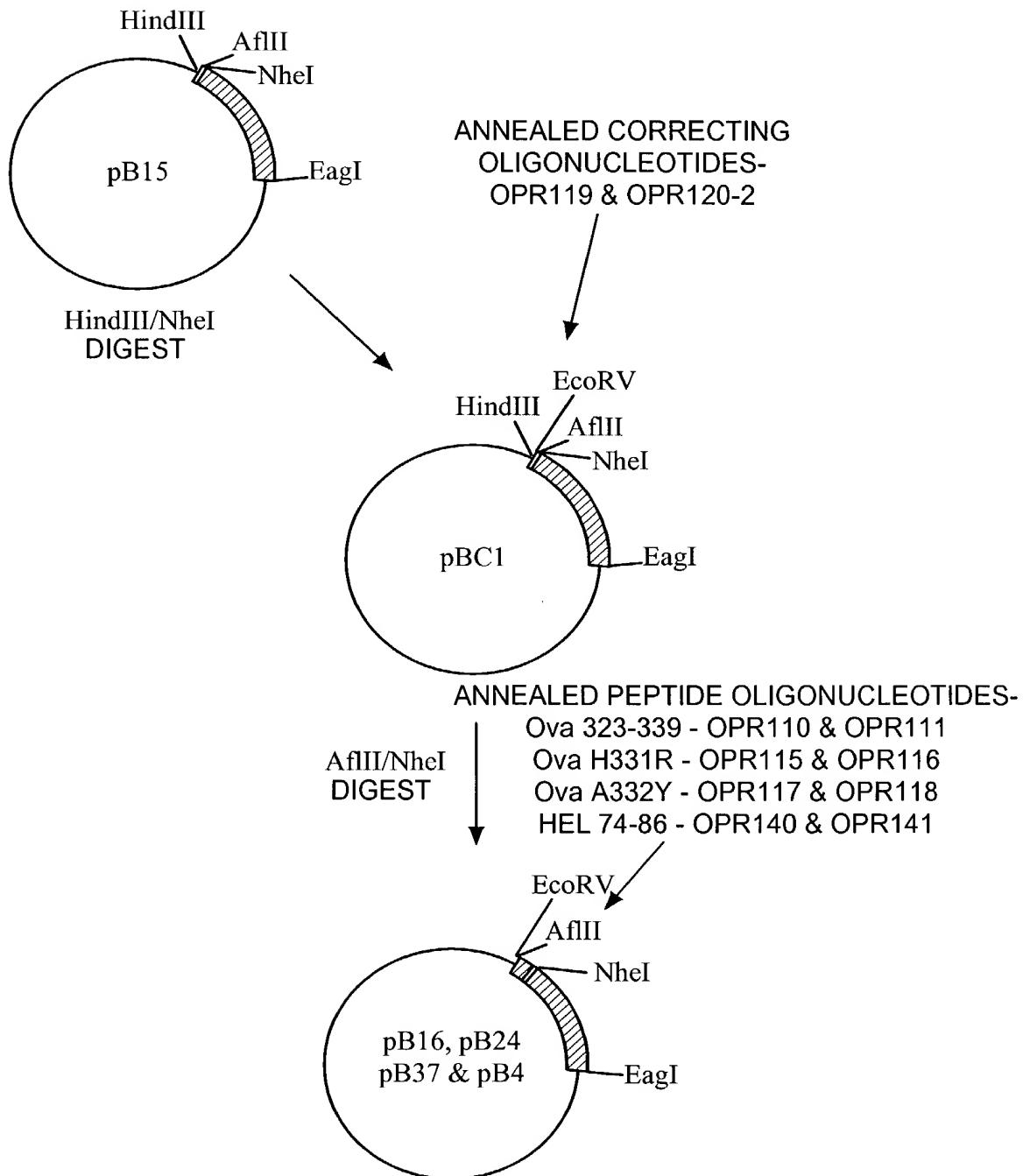


FIG. 3B

HLA-DRI α CHAIN CLONING SCHEME

TOTAL RNA ISOLATED
FROM BLCL K68 CELLS

SYNTHESIS OF FIRST STRAND cDNA USING OLIGO-dT PRIMER

TEMPLATE

PCR AMPLIFICATION WITH DR1A-B & DR1A-F PRIMERS

**α1 - α2-HINGE
PCR PRODUCT**

**HindIII/BamHI
DIGEST**

Diagram of a circular cell with a hatched region on the right side. An arrow points to the hatched region with the label "HindIII".

BamHI

TEMPLATE FOR PCR AMPLIFICATIONS

FIG. 4A

FIG. 4B

FIG. 4

PCR WITH AF-N & AB-S PRIMERS

α_1 - α_2 -HINGE
PCR PRODUCT

NcoI/SpeI DIGEST

39A2

TEMPLATE FOR PCR AMPLIFICATIONS

FIG. 4A

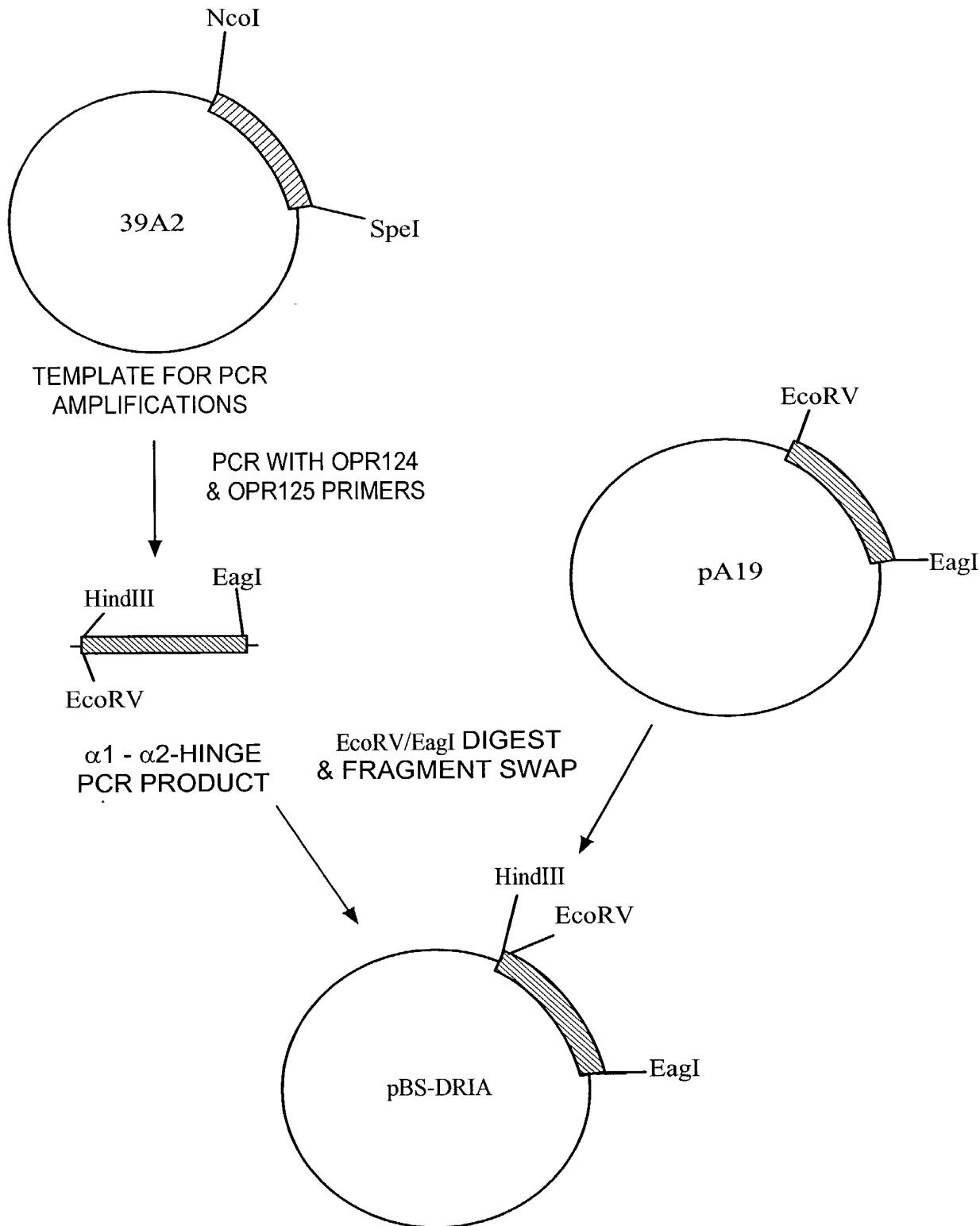
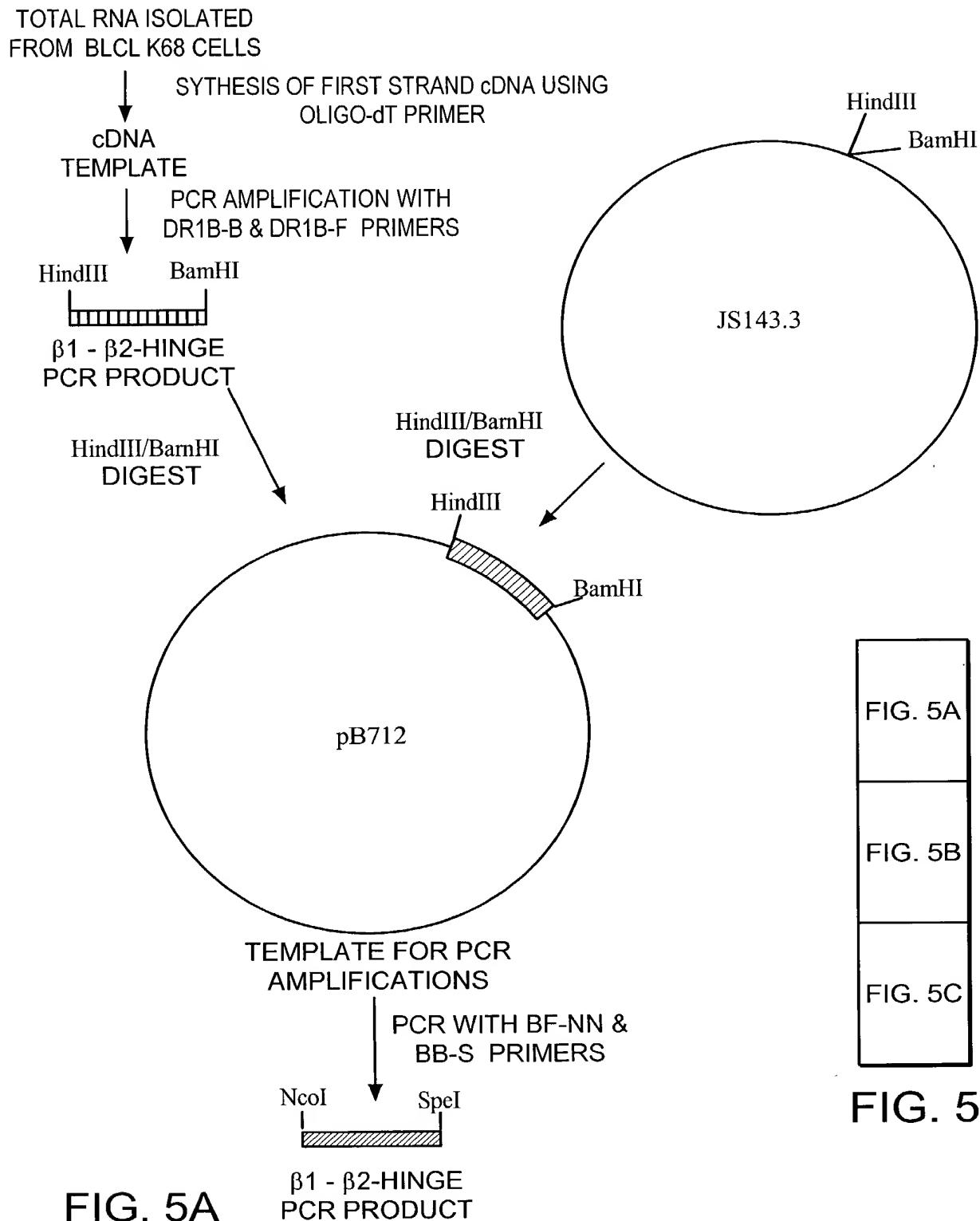


FIG. 4B

HLA-DRI β CHAIN CLONING SCHEME



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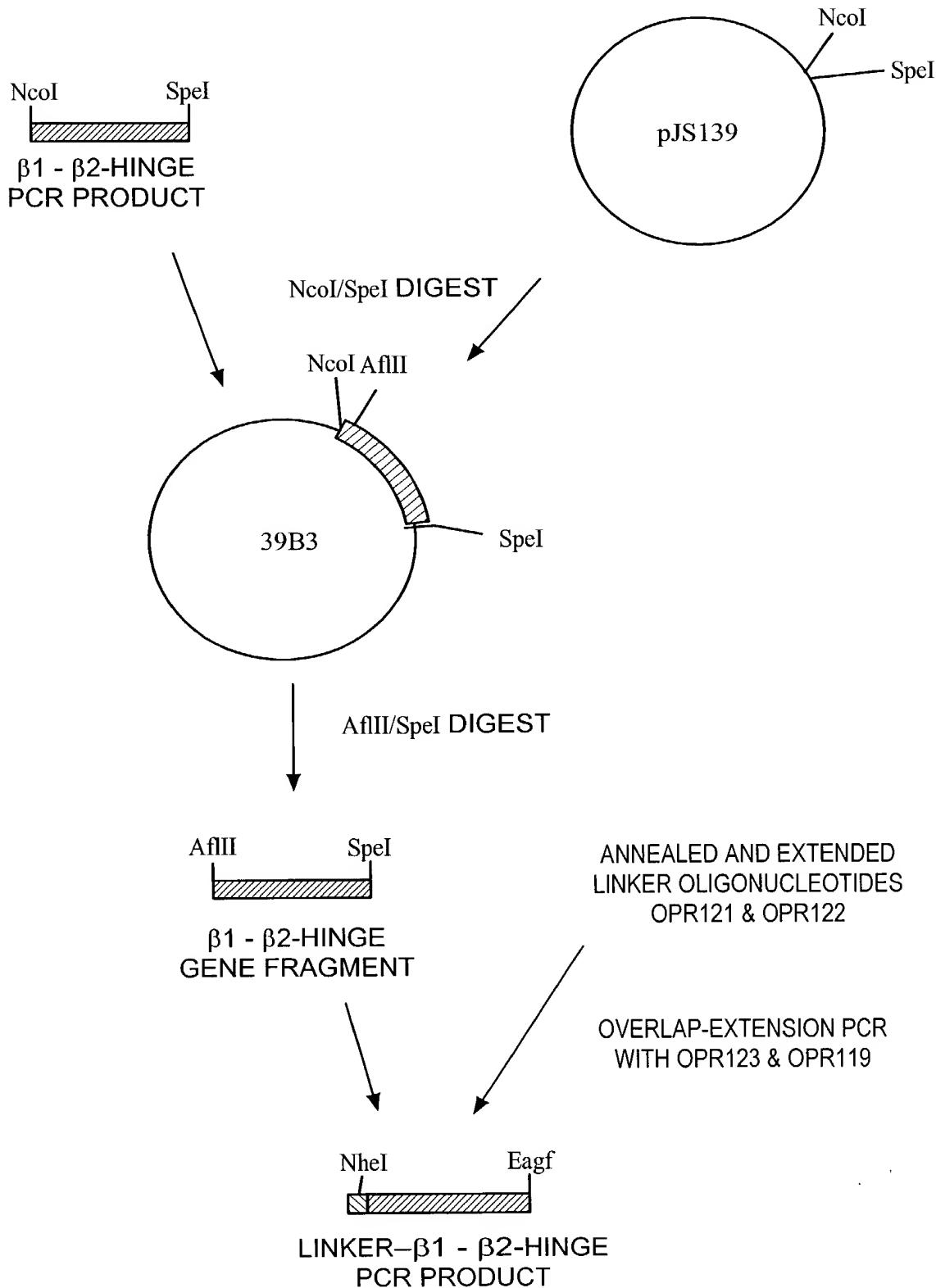


FIG. 5B

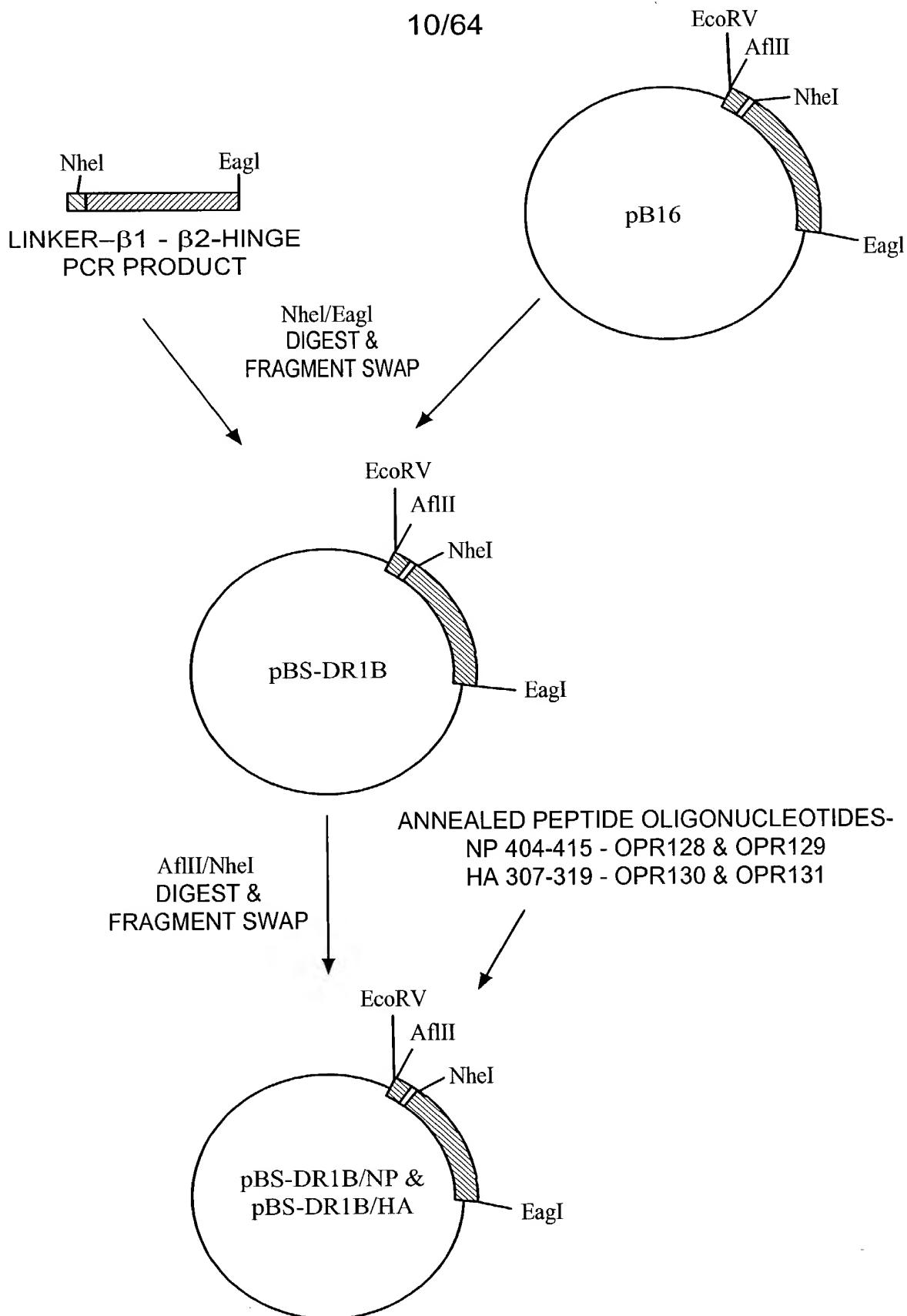


FIG. 5C

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I-A^S α CHAIN CLONING SCHEME

TOTAL RNA ISOLATED FROM
SJL MOUSE SPLEEN CELLS

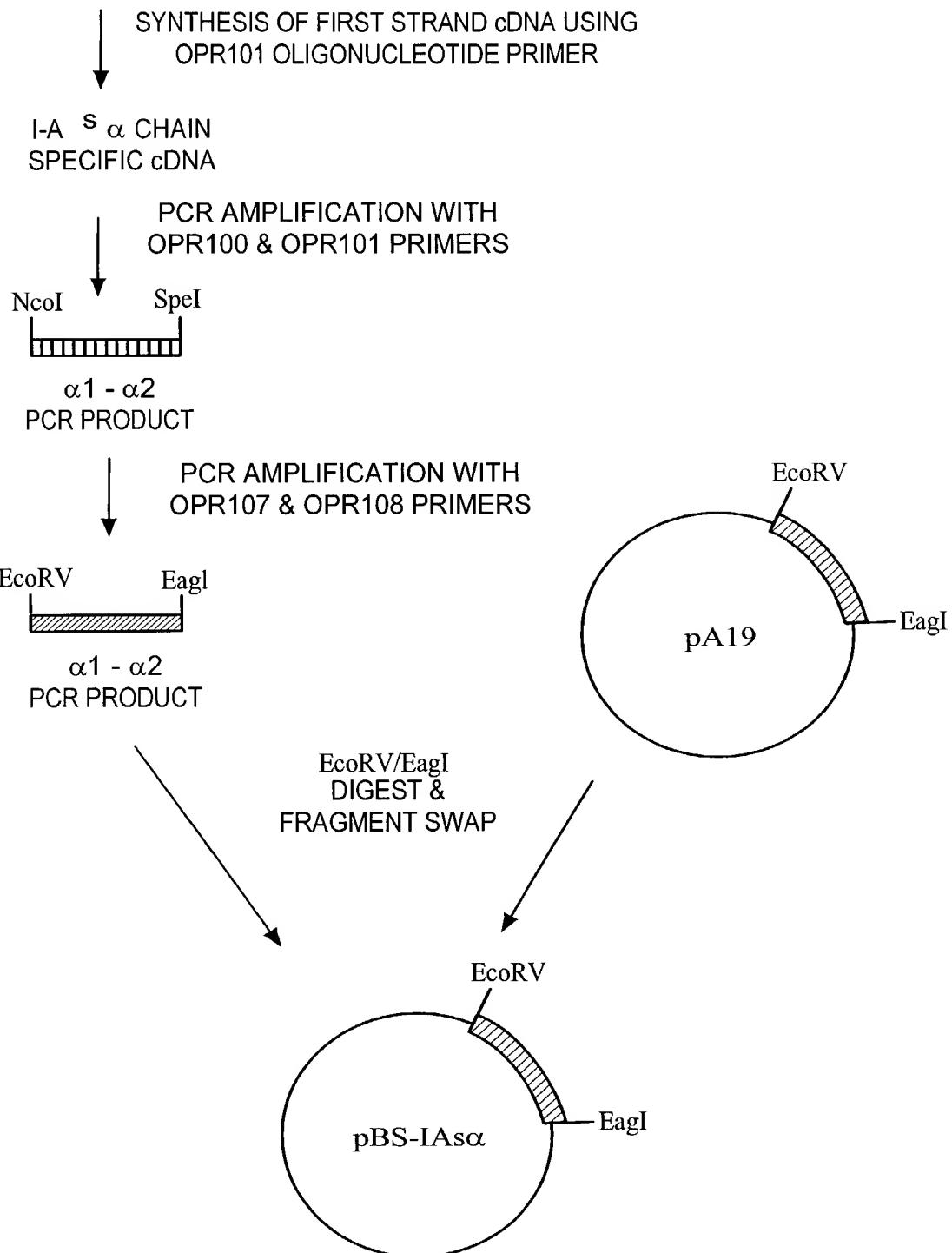


FIG. 6

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FIG. 8A

FIG. 8B

FIG. 8C

FIG. 8D

FIG. 8

I-A^S β CHAIN CLONING SCHEME

TOTAL RNA ISOLATED FROM
 SJL MOUSE SPLEEN CELLS

↓
 SYNTHESIS OF FIRST STRAND cDNA USING
 OPR106 PRIMER
 I-A^S β CSPECIFIC
 cDNA TEMPLATE

↓
 PCR AMPLIFICATION WITH
 VW310 & OPR106 PRIMERS

↓
 β1 - β2
 PCR PRODUCT

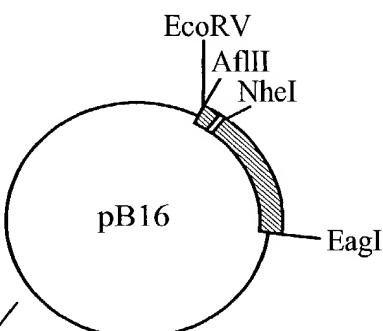
↓
 PCR AMPLIFICATION WITH
 VW309 & OPR106 PRIMERS

↓
 NheI EagI
 LINKER-
 β1 - β2
 PCR PRODUCT

NheI/EagI
 DIGEST &
 FRAGMENT SWAP

EcoRV AfI^{III}
 NheI

pBS-IAsβ



NheI/EagI
 DIGEST

EagI

ANNEALED PEPTIDE OLIGONUCLEOTIDES-
 MBP 91-103 - VW315 & VW316
 PLP 139-151 - VW313 & VW314
 MBP 1-14 - VW317 & VW318

AfI^{III}/NheI
 DIGEST &
 FRAGMENT SWAP

EcoRV AfI^{III}
 NheI

pBS-IAsβ/MBP91,
 pBS-IAsβ/PLP &
 pBS-IAsβ/MBPI

FIG. 7

OLIGOMICROLEOTIDES USED IN CONSTRUCTING MHC VECTORS

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I-A^d/I-A^s PCR PRIMERS AND CLONING OLIGONUCLEOTIDES
(RESTRICTION SITES ARE UNDERLINED)

OPR100

5' -GGG GGG GCC ATG GCC GAA GAC GAC ATT GAG GCC GAC-3'

OPR101

5' -GGG GGG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107

5' -CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG
GCC G-3'

OPR108

5' -CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG
C-3'

OPR102

5' -GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104

5' -GCG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106

5' -CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112

5' -CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC
GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119

5' -AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'

OPR120-2

5' -CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310

5' -TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309

5' -CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136

5' -CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

5' -CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

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OPR132

5'-CCC CCC AAG CTT CCC GGG CGA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

HLA-DR1 PCR PRIMERS AND CLONING OLIGONUCLEOTIDES

DR1A-F

5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DR1A-B

5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DR1B-F

5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG
CAG C-3'

AF-N

5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S

5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124

5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA
GAA GAA CAT GTG ATC-3'

OPR125

5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG
AGC-3'

DR1B-B

5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN

5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA
CGT TTC TTG-3'

BB-5

5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

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OPR121

5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT
GGT GGG GAC ACC CG-3'

OPR122

5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG
GGT GTC CCC ACC ACC-3'

OPR123

5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-
3'

PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339

OPR110

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR111

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

HEL 74-86

OPR140

5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC
TCC G-3'

OPR141

5'-CTA GCG GAG CTC AGC AGG GCG CTG CAGBGGG ATG TTG CAC AGG
TTA C-3'

FIG. 8C

Title: MHC Complexes And Uses Thereof
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NP 404-415

OPR129

5' -TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

OPR129

5' -CTA GCC TGC ACG CTG AAG GCG GGC TEA ACG CTG ATC TGA C-3'

HA 307-319

OPR130

5' -TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC
ACC G-3'

OPR131

5' -CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG
GGA C-3'

MBP 91-103

VW315

5' -TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG
CGC G-3'

VW316

5' -CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG
TGA C-3'

PLP 139-151

VW313

5' -TTA CAC CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG
TTC G-3'

VW314

5' -CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG
TGA C-3'

MBP 1-14

VW317

5' -TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG
TAC CTG G-3'

VW316

5' -CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT
GCC ATA C-3'

FIG. 8D

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
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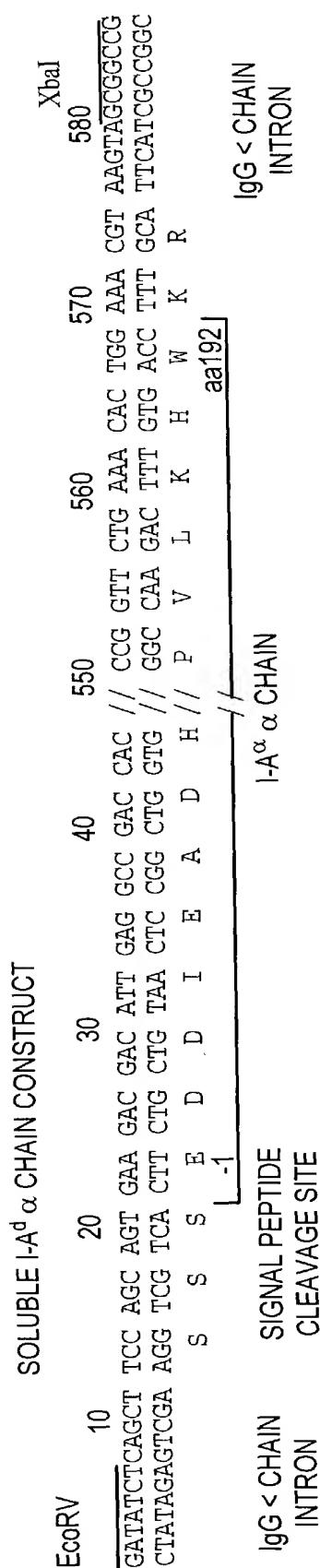
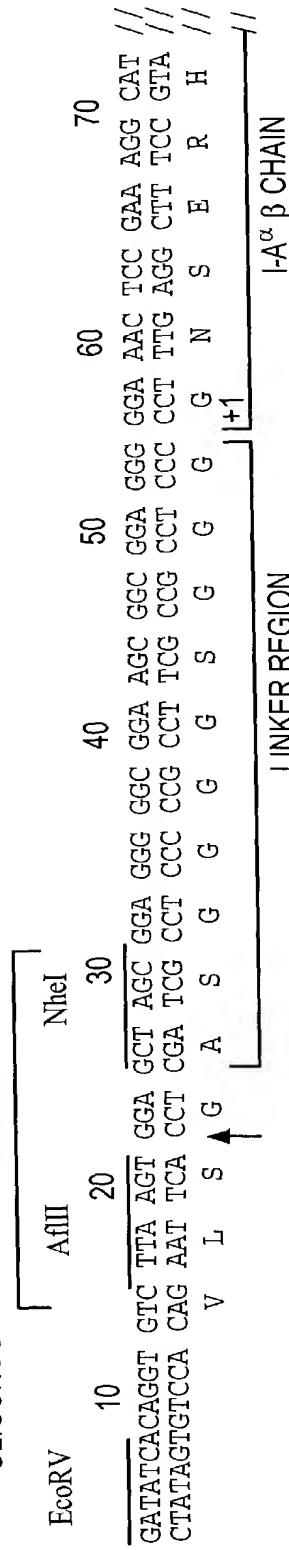


FIG. 9A

RESTRICTION SITES FOR INSERTION OF
OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



IgG H CHAIN
INTRON

610	620	630
ATC ACT GTG GAG TGG TCC TCA GGT	ACGGGGCC	
TAG TGA CAC CTC ACC AGG AGT CCA	TGCCGGCC	
L T V E W S S		
aaL89		

FIG. 9B

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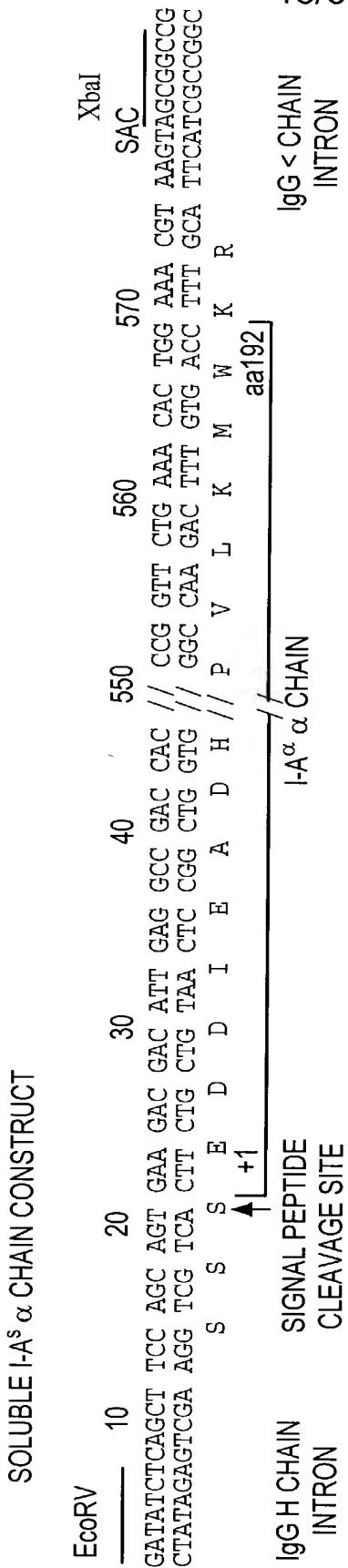
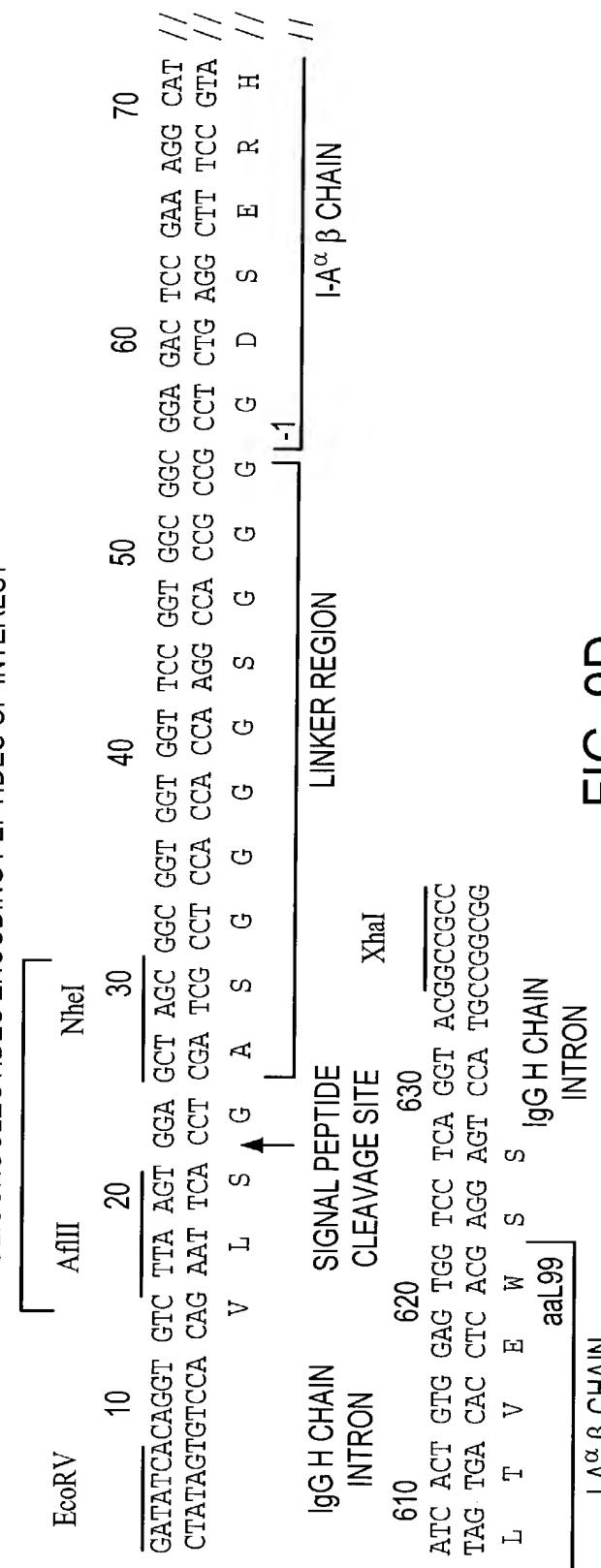


FIG. 9C

SOLUBLE I-AS^S β CHAIN CONSTRUCT
 RESTRICTION SITES FOR INSERTION OF
 OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

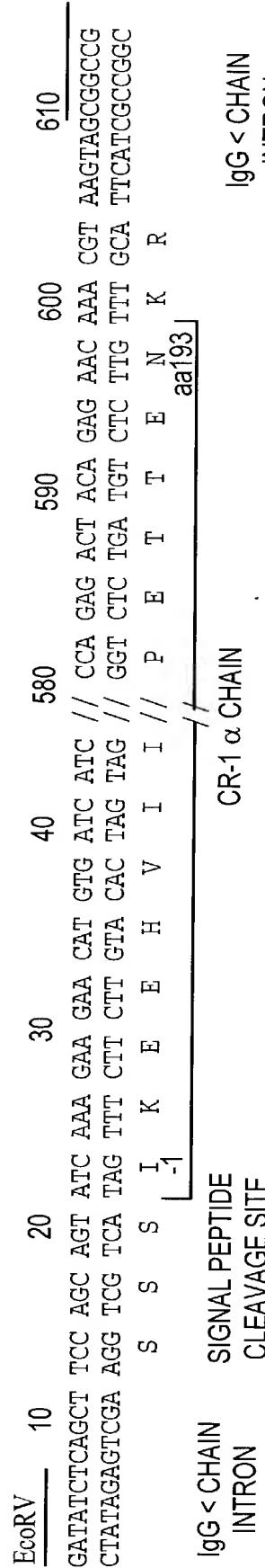


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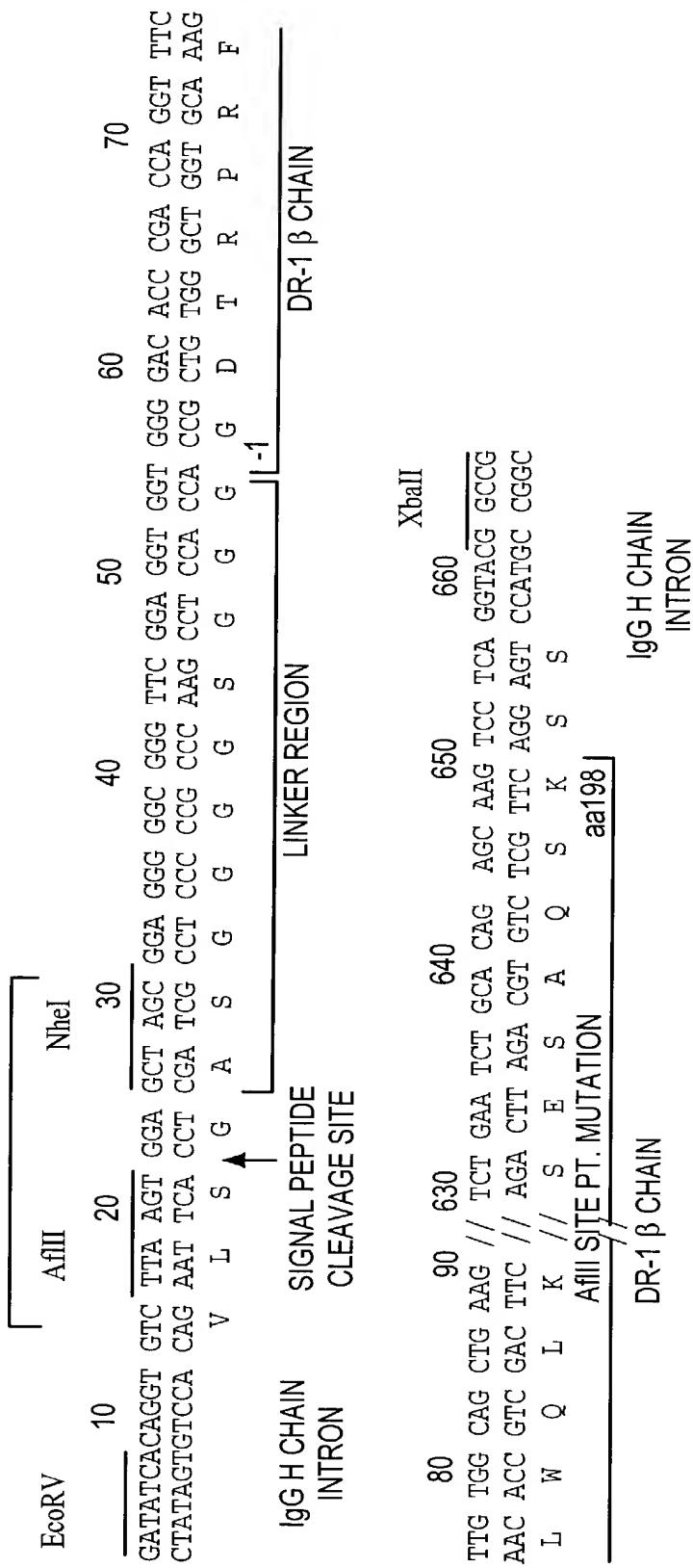
SOLUBLE HLA-DR1 α CHAIN CONSTRUCT



IgG < CHAIN
 INTRON

FIG. 9E

SOLUBLE HLA-DR1 β CHAIN CONSTRUCT
 RESTRICTION SITES FOR INSERTION OF
 OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
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FIG. 9F

Title: MHC Complexes And Uses Thereof
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ORIGINAL MAMMALIAN CELL EXPRESSION VECTORS

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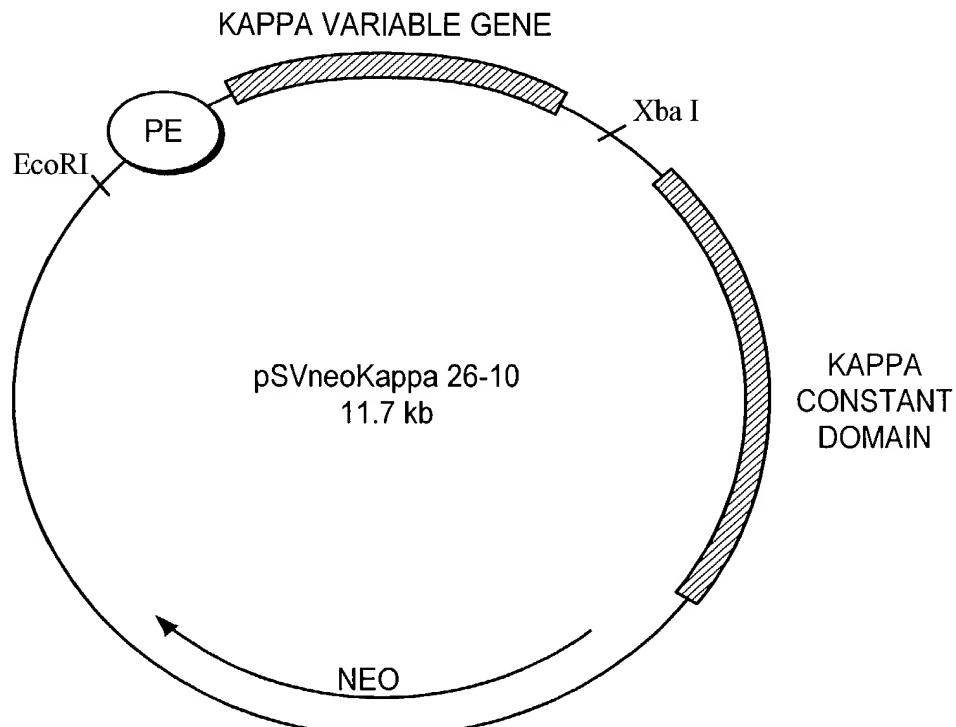


FIG. 10A

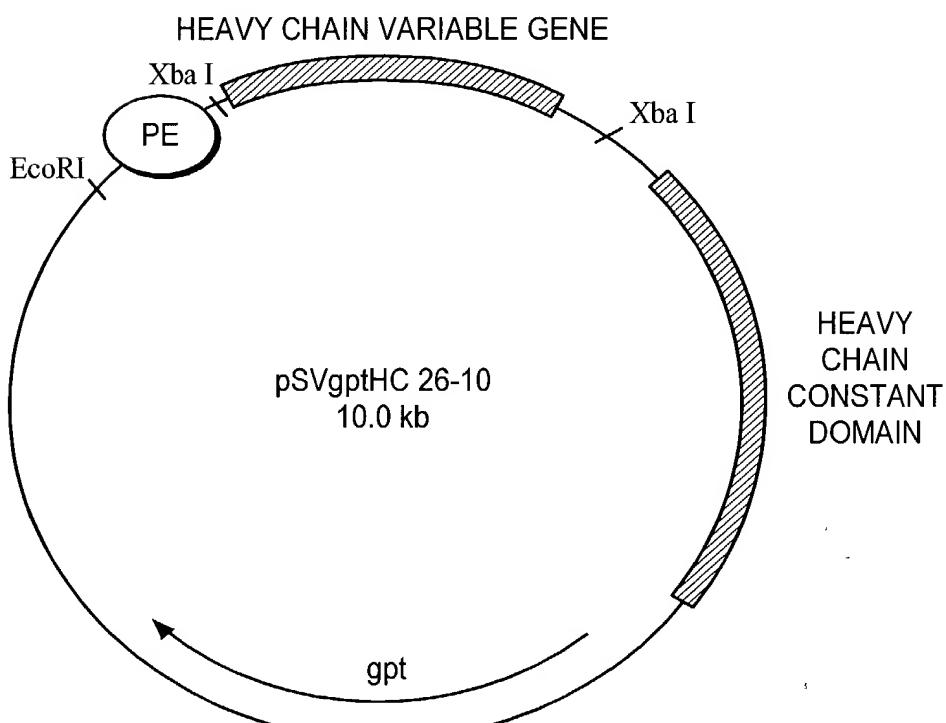


FIG. 10B

THE 2.7 Kb KAPPA AND THE 1.7 Kb HEAVY CHAIN/EcoRV AND Eag I. MUTATED CONSTRUCTS

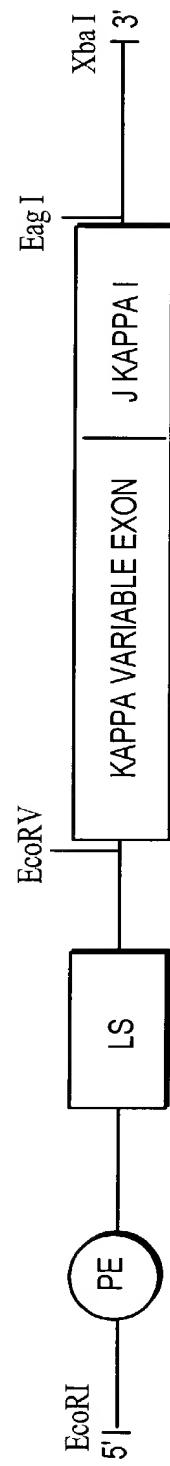


FIG. 11A



FIG. 11B

Title: MHC Complexes And Uses Thereof
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PCR SITE DIRECTED MUTAGENESIS FOR INTRODUCING EcoRV and EagI RESTRICTION SITES INTO KAPPA CHAIN 2.7 kb INSERT

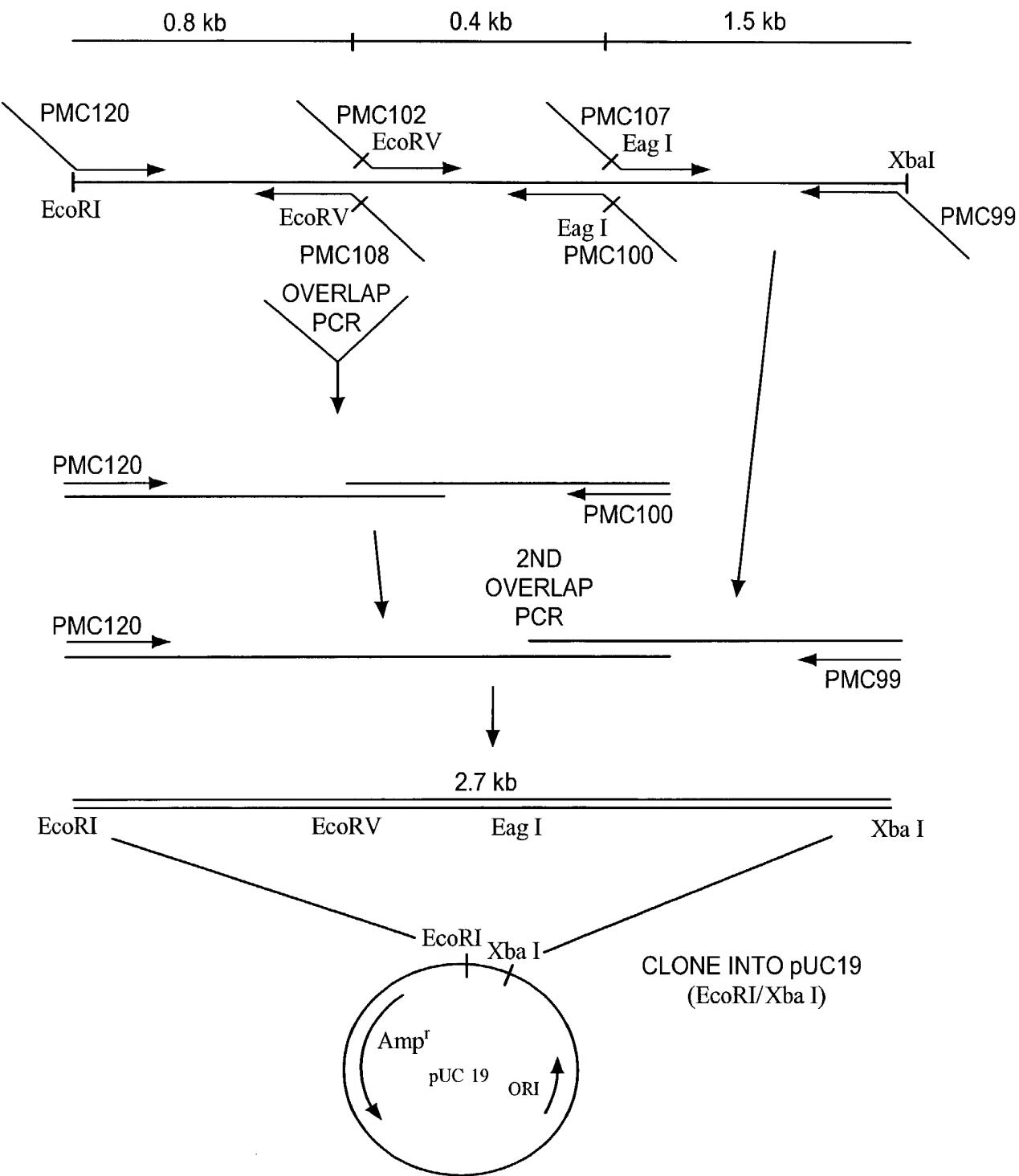


FIG. 12

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STRATEGY FOR CONSTRUCTING MHC CLASS IIc/KAPPA CONSTANT GENE IN MAMMALIAN CELL EXPRESSION VECTOR

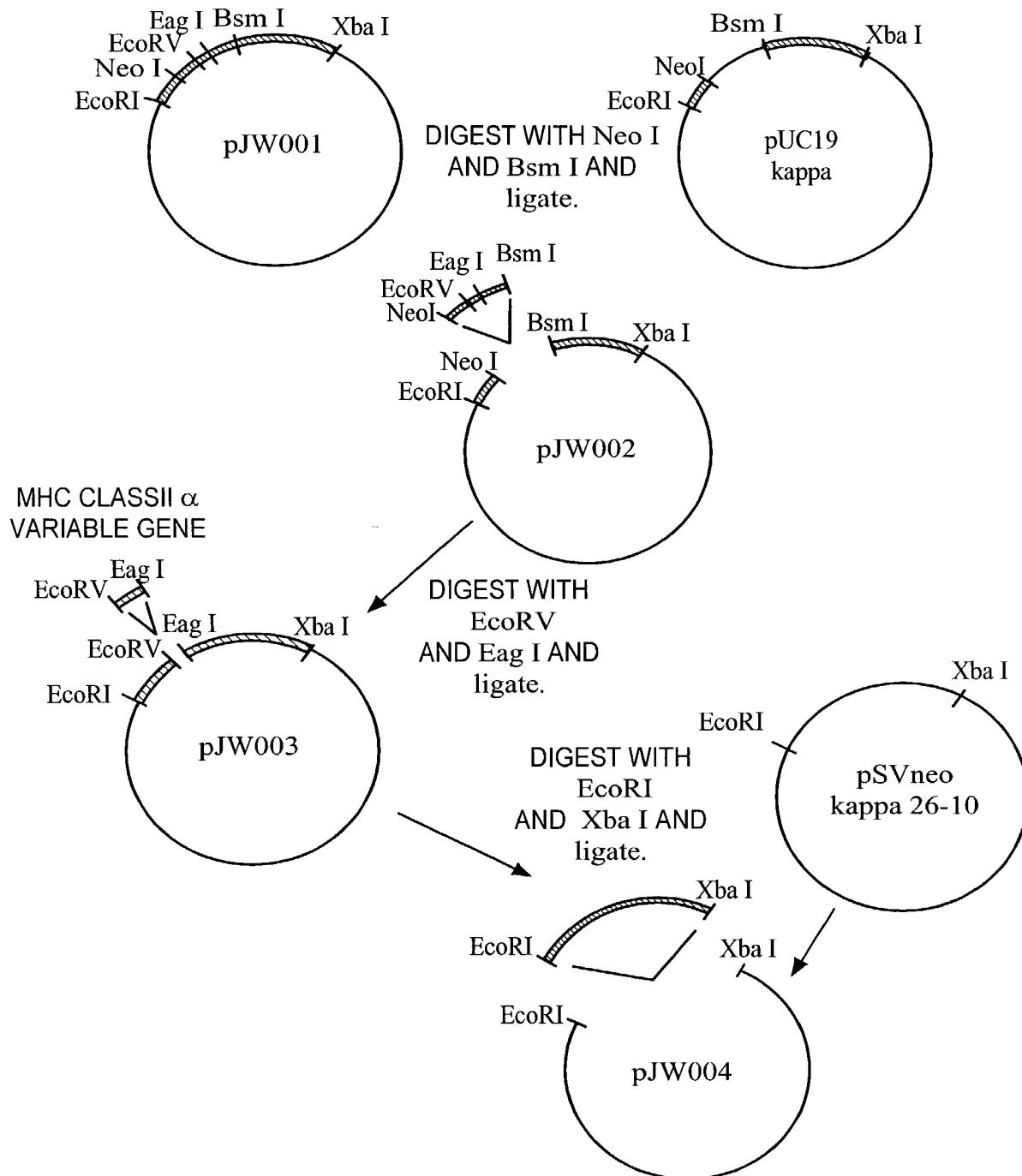


FIG. 13

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PRIMERS USED FOR SEQUENCING MUTATED 2.7Kb FRAGMENT

PRIMER LIST

<u>PRIMER LIST</u>	<u>SEQUENCE</u>
PMC-33	(5' GCTCAGGCTGTCTTGTCTTCACTGATC3')
PMC-77	(5' GTAAAGTAGGGCCG3')
PMC-111	(5' GGTATGTAATAAACATCACAG3')
PMC-114	(5' GCTTGGCTTACGGAGTTACTC3')

FIG. 14

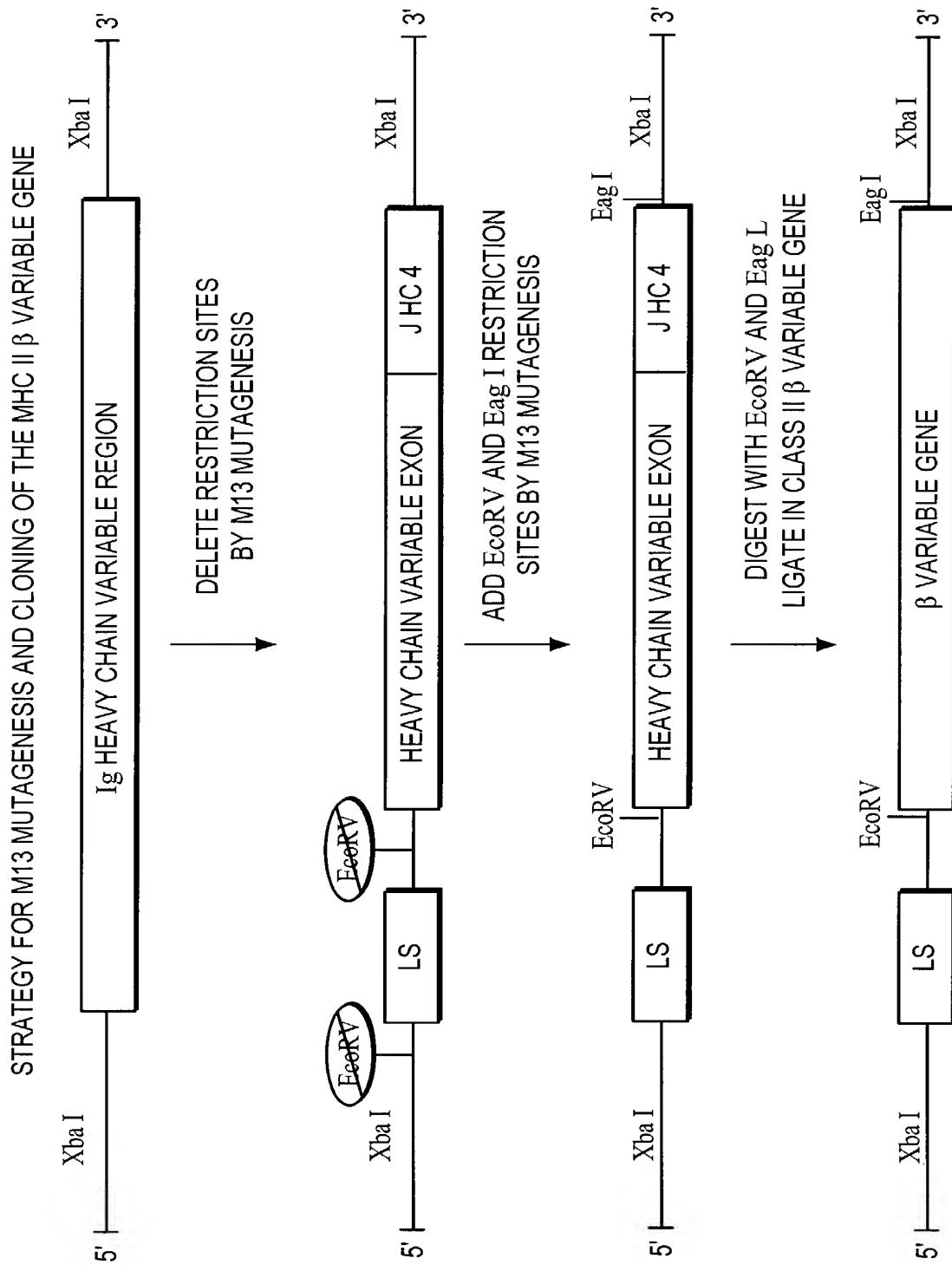


FIG. 15

Title: MHC Complexes And Uses Thereof
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FINAL VECTORS FOR EXPRESSING MHC II/Ig CHIMERIC PROTEINS

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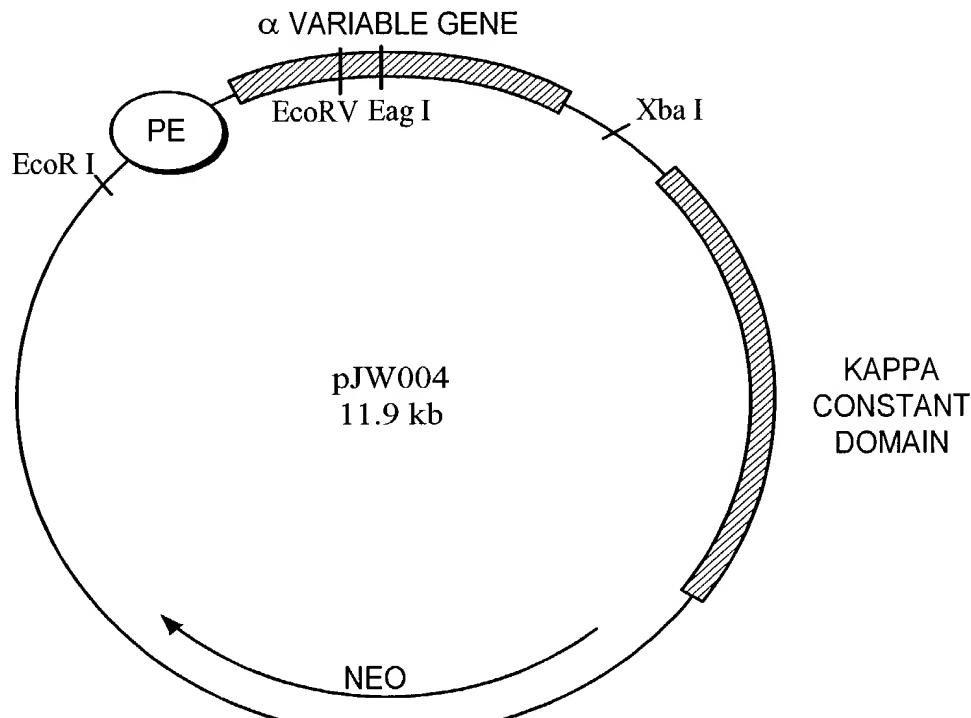


FIG. 16A

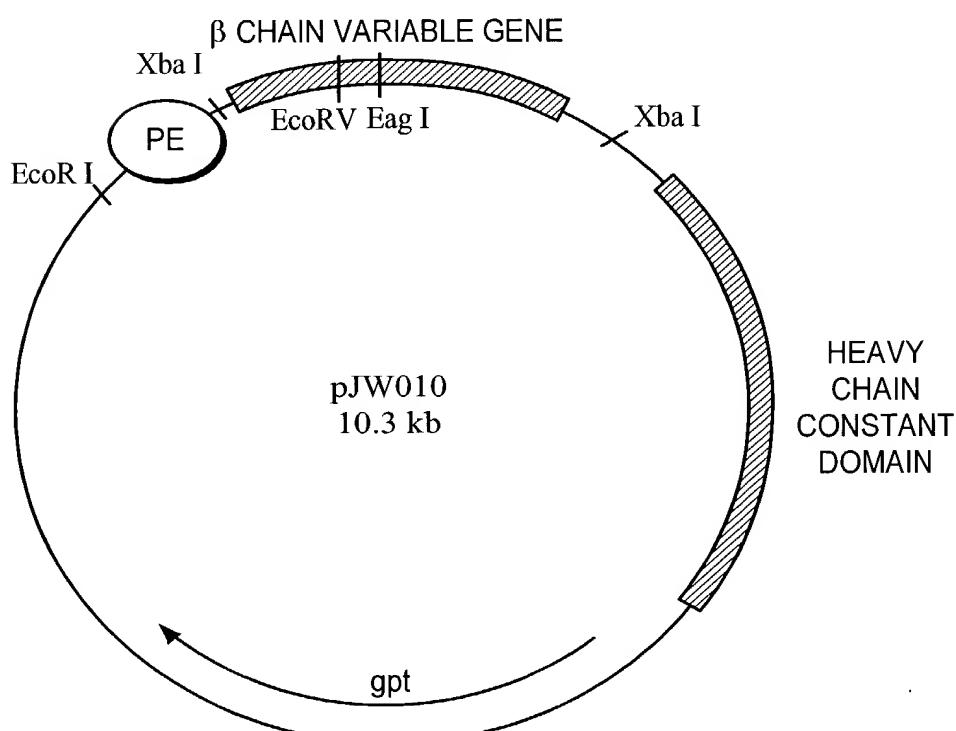


FIG. 16B

FIG. 17A

FULL LENGTH PEPTIDE LINKED MHC EXPRESSION VECTORS

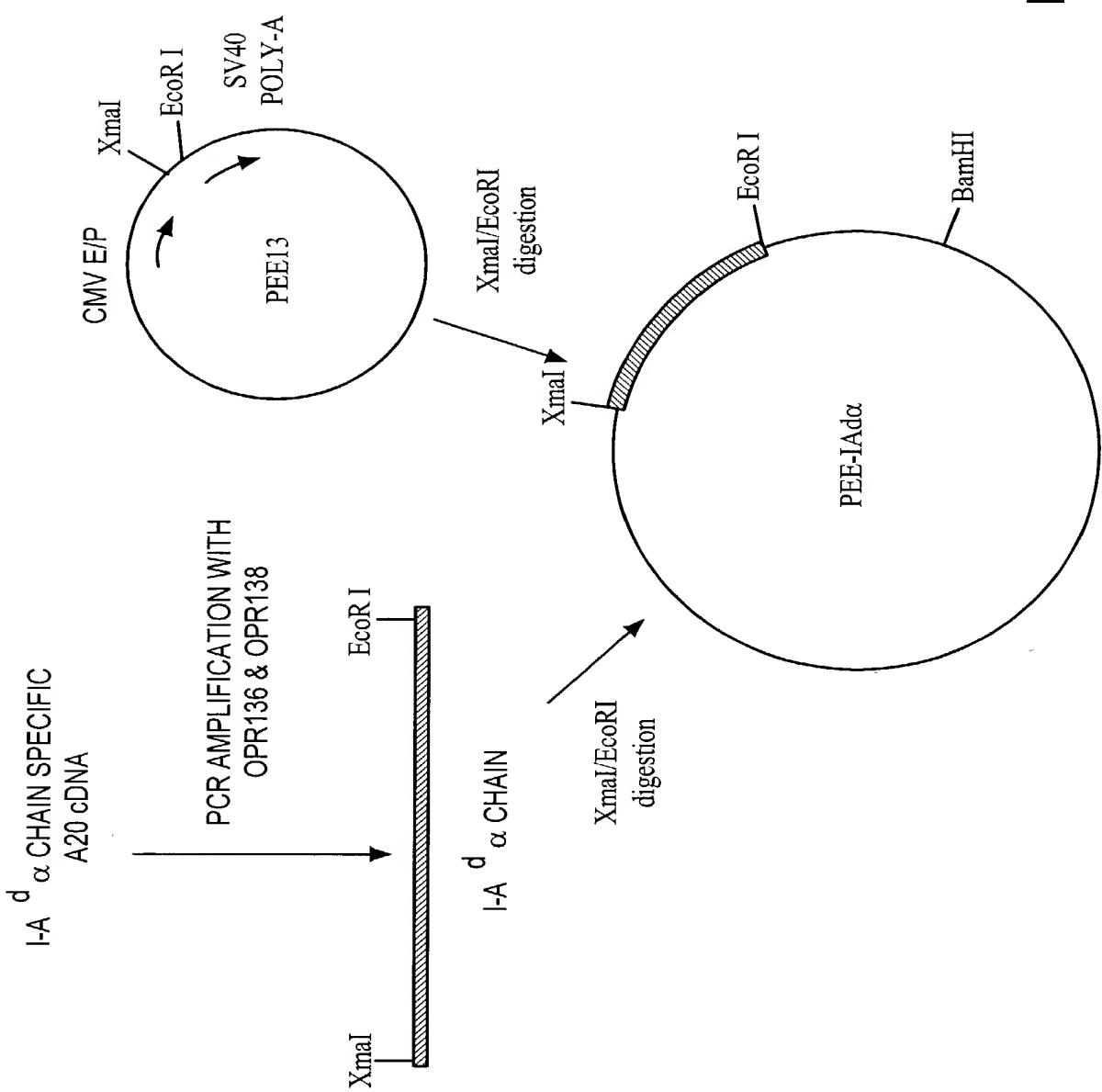


FIG. 17

FIG.
17BFIG.
17C

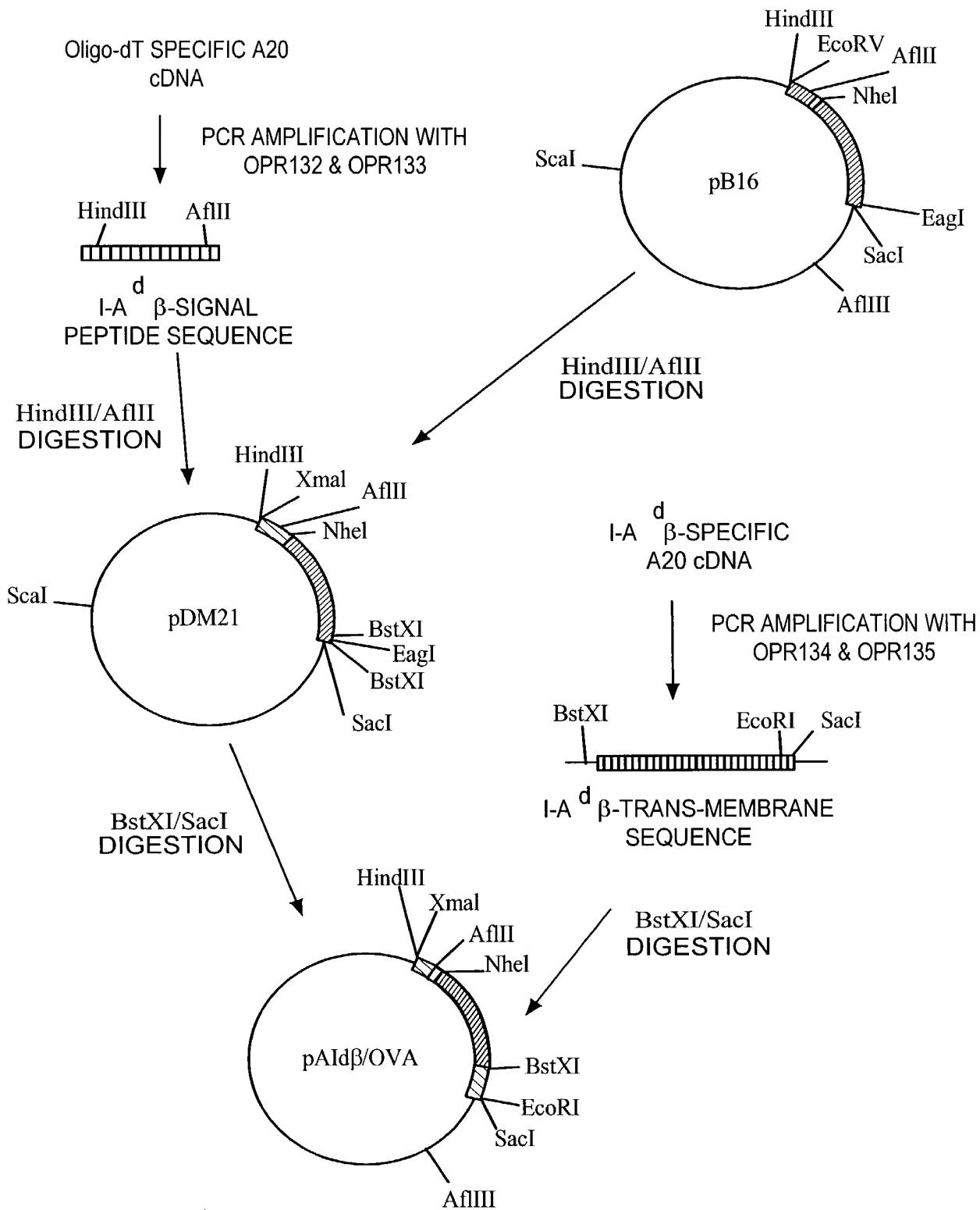


FIG. 17B

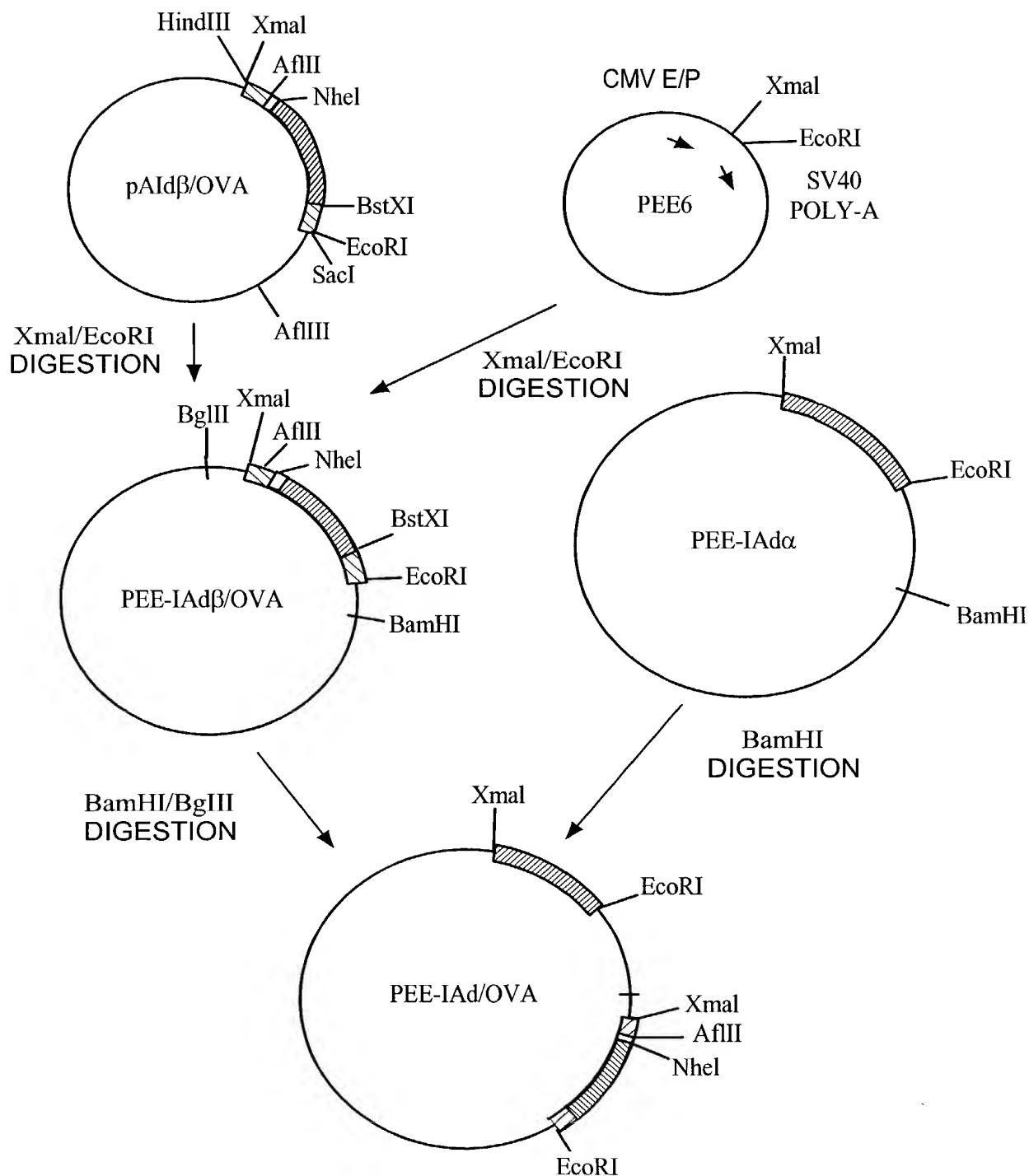


FIG. 17C

FULL LENGTH I-A^d α CHAIN INSERT

Xhaf	10	20	30	40	50									
CCCGGGCCAC	C	ATG	CCG	TGC	AGC	AGA	GCT	CTG	ATT	CTG	GGG	GTC	CTC	GCC
GGGCCCGGTG	G	TAC	GGC	ACG	TCG	TCT	CGA	GAC	TAA	GAC	CCC	CAG	GAG	CGG
	M	P	C	S	R	A	L	I	L	G	V	L	A	

KOZAK
CONSENSUS I-A^d α CHAIN SIGNAL PEPTIDE

60	70	80	90
CTG AAC ACC ATG CTC AGC CTC TGC GGA GGT GAA GAC GAC ATT GAG //	GAC TTG TGG TAC GAG TCG GAG ACG CCT CCA CTT CTG CTG TAA CTC //		
L N T M L S L C G G		E	O O I E //
			
I-A^d α CHAIN SIGNAL PEPTIDE			
SIGNAL PEPTIDE			
CLEAVAGE SITE			

EcoRI

750	760	770	780
CGA TCA GGT GCC ACC TCC AGA CAC CCA GGG CCT TTA TGA	GAATTC		
GCT AGT CCA CCG TGG AGG TCT GTG GGT CCC GGA AAT ACT	GTAAAG		
R S G G T S R H P G P L -			
			stop

I-A^d α CHAIN

FIG. 18A

09000379 061307b

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FULL LENGTH I-A^d β CHAIN INSERT

HindIII Xhaf	10	20	30	40	50								
AAGCTTCCCG	GGCCACC	ATG	GCT	CTG	CAG	ATC	CCC	AGC	CTC	CTC	CTC	TCA	GCT
TTCGAAGGGC	CCGGTGG	TAC	CGA	GAG	GTC	TAG	GGG	TCG	GAG	GAG	GAG	AGT	CGA
	M	A	L	Q	I	P	S	L	L	L	S	A	

KOZAK CONSENSUS I-A^d β CHAIN SIGNAL PEPTIDE

	110		120		130		140								
TCT	CAG	GCT	GTT	CAC	GCT	GCT	CAC	GCT	GAA	ATC	AAC	GAA	GCT	GGT	CGT
AGA	GTC	CGA	CAA	GTG	CGA	CGA	GTG	CGA	CTT	TAG	TTG	CTT	CGA	CCA	GCA
S	Q	A	V	H	A	A	H	A	C	I	H	L	A	G	R

QVF PEPTIDE

870	880	890	900	EcoRI	SacI					
CCT	CCT	CCA	GCA	GGG	CTC	CTG	CAG	TGA	GAAT	TCCAGCTC
GGA	GGA	GGT	CGT	CCC	GAG	GAC	GTC	ACT	CTTA	AGCTCGAG
P	P	P	A	G	L	L	Q	—		
stop										
I-A^d β CHAIN										

FIG. 18B

Title: MHC Complexes And Uses Thereof
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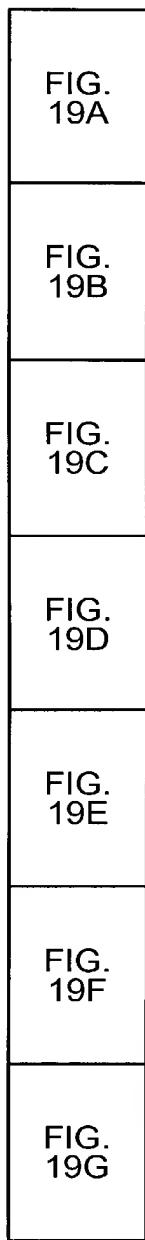


FIG. 19

FULL-LENGTH PEPTIDE LINKED MHC EXPRESSION VECTORS

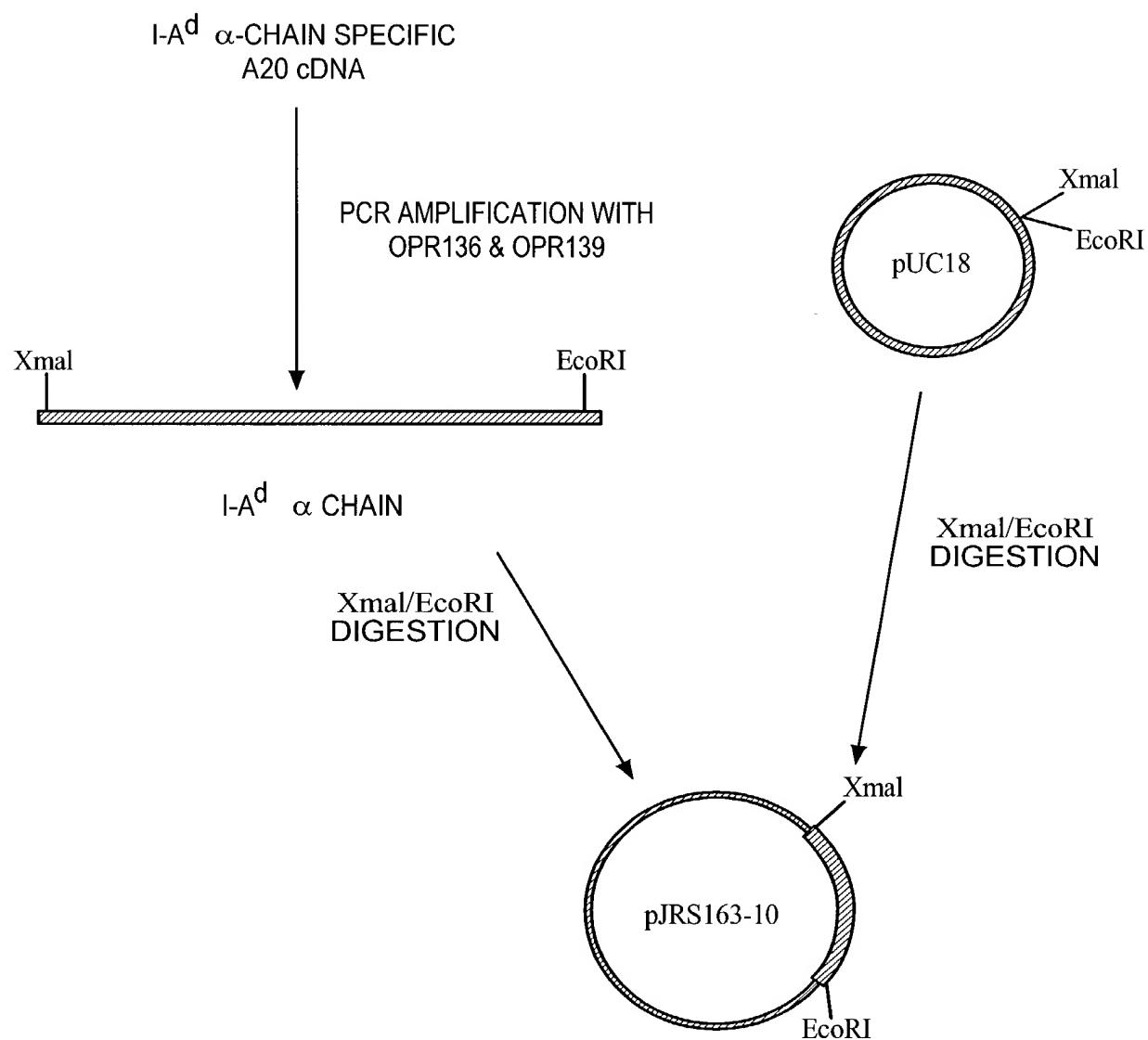


FIG. 19A

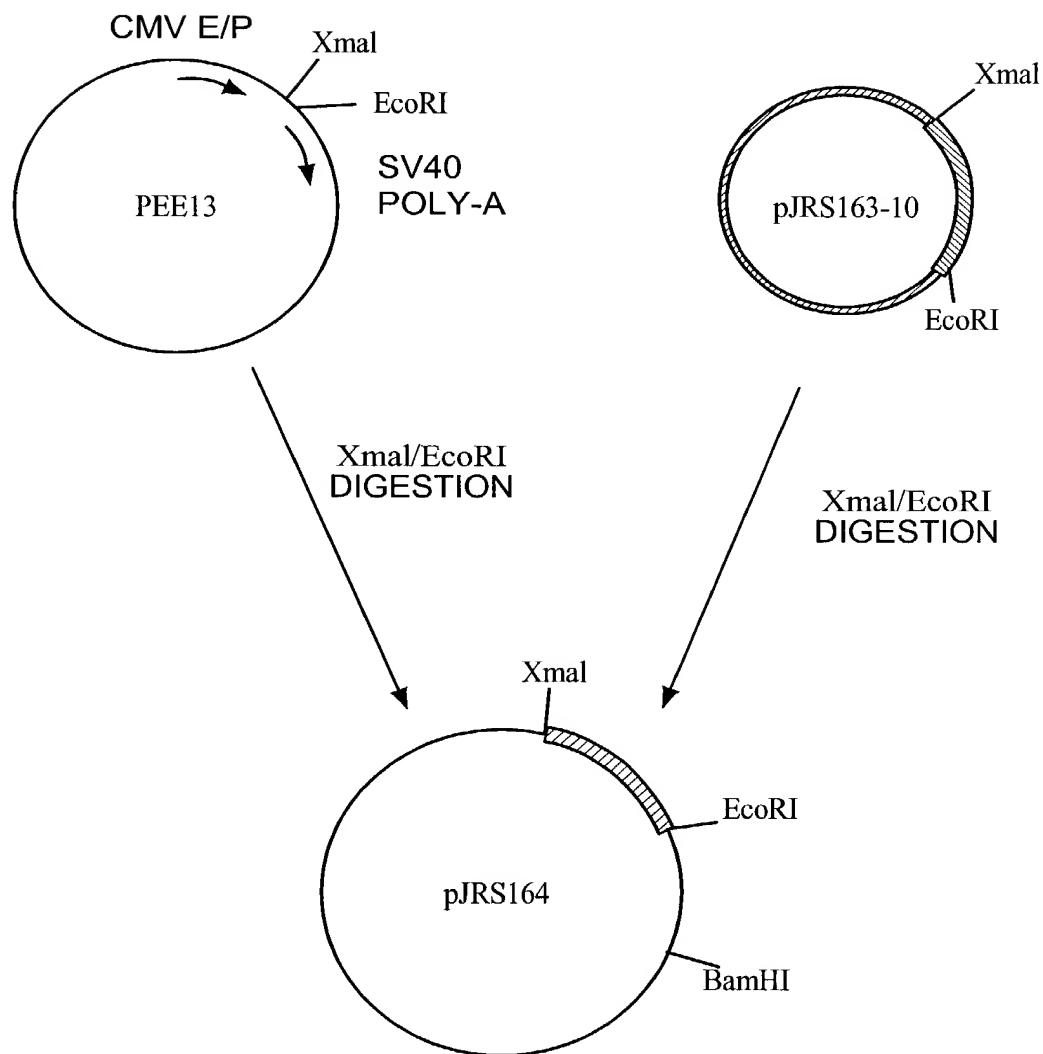


FIG. 19B

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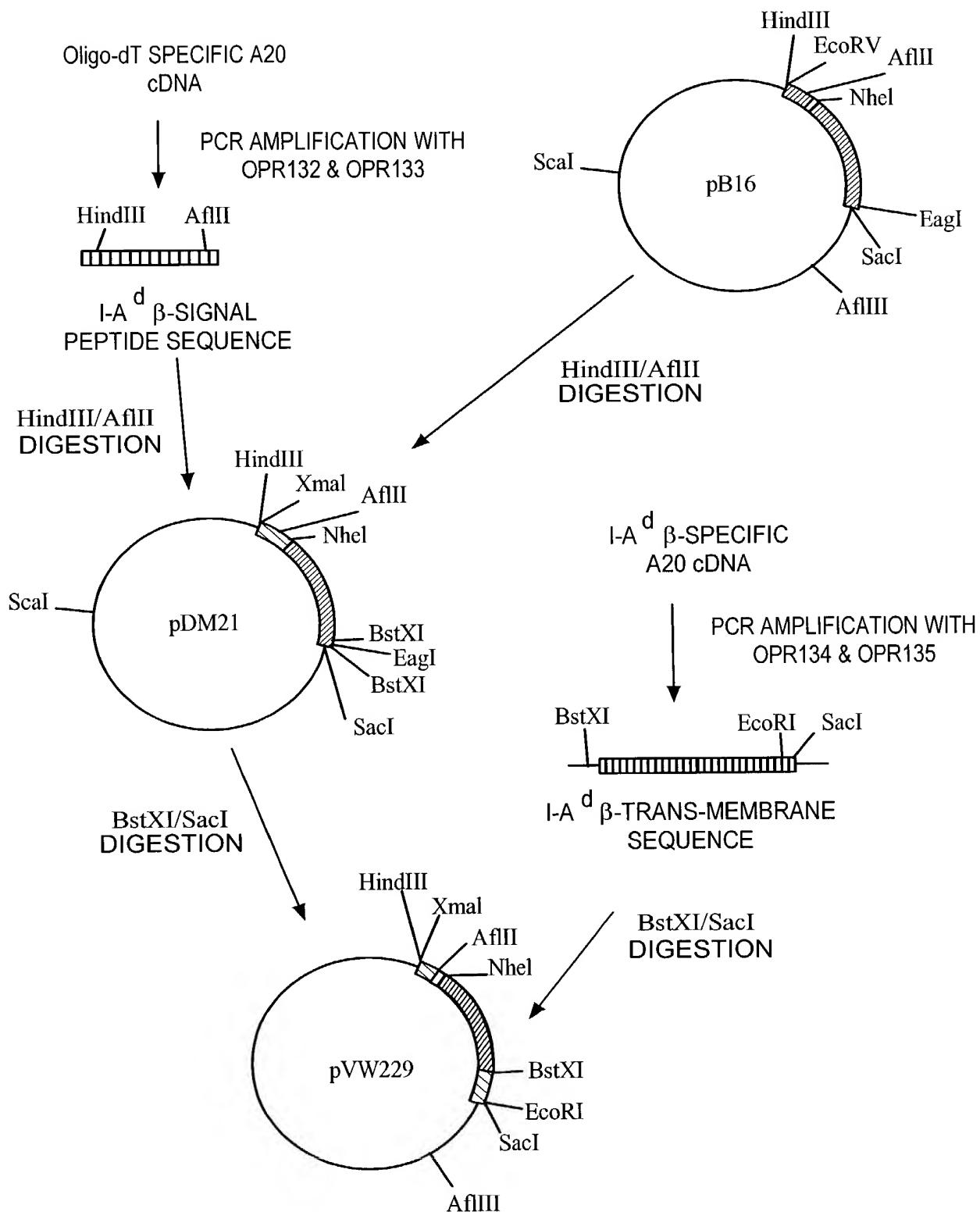


FIG. 19C

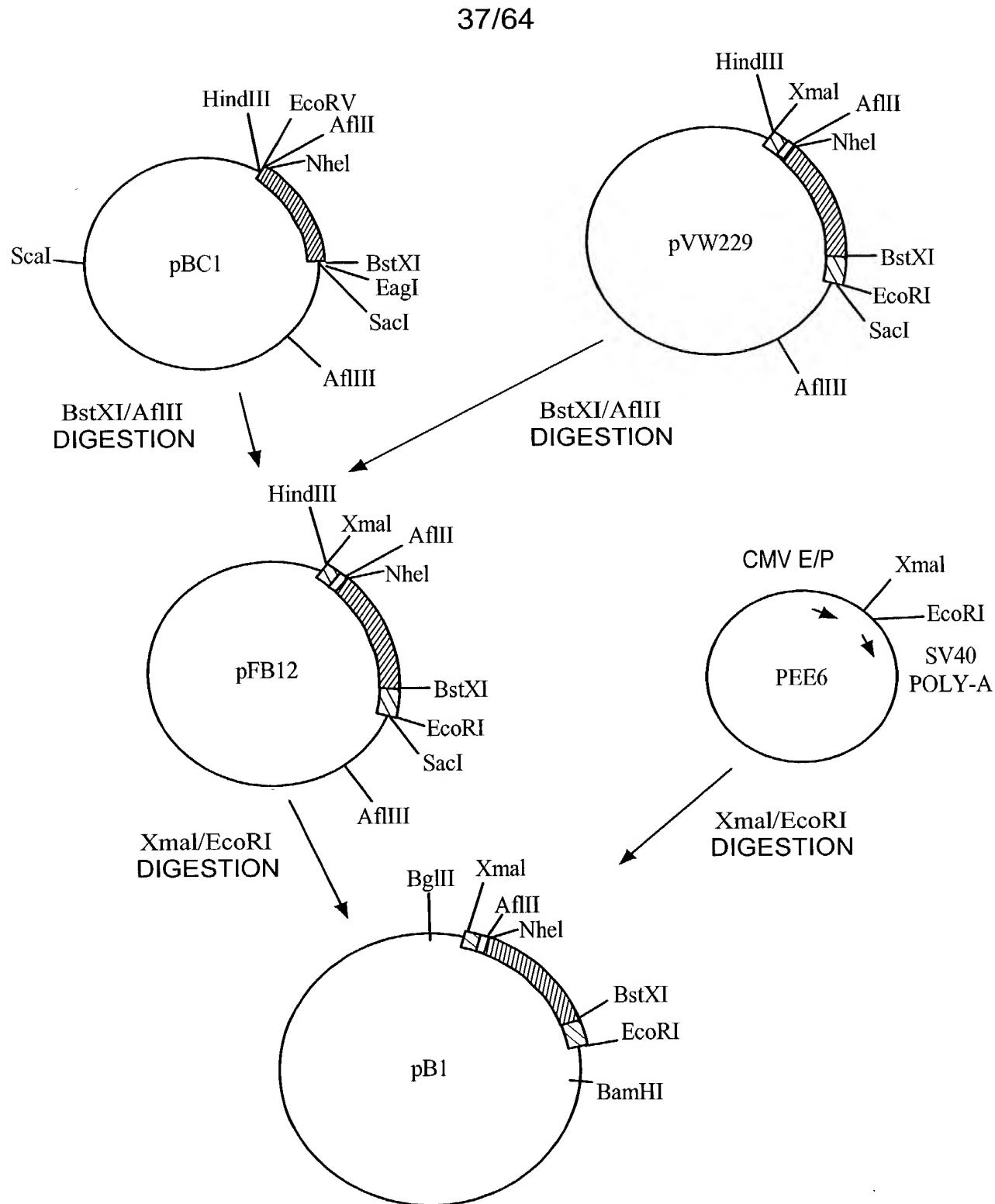


FIG. 19D

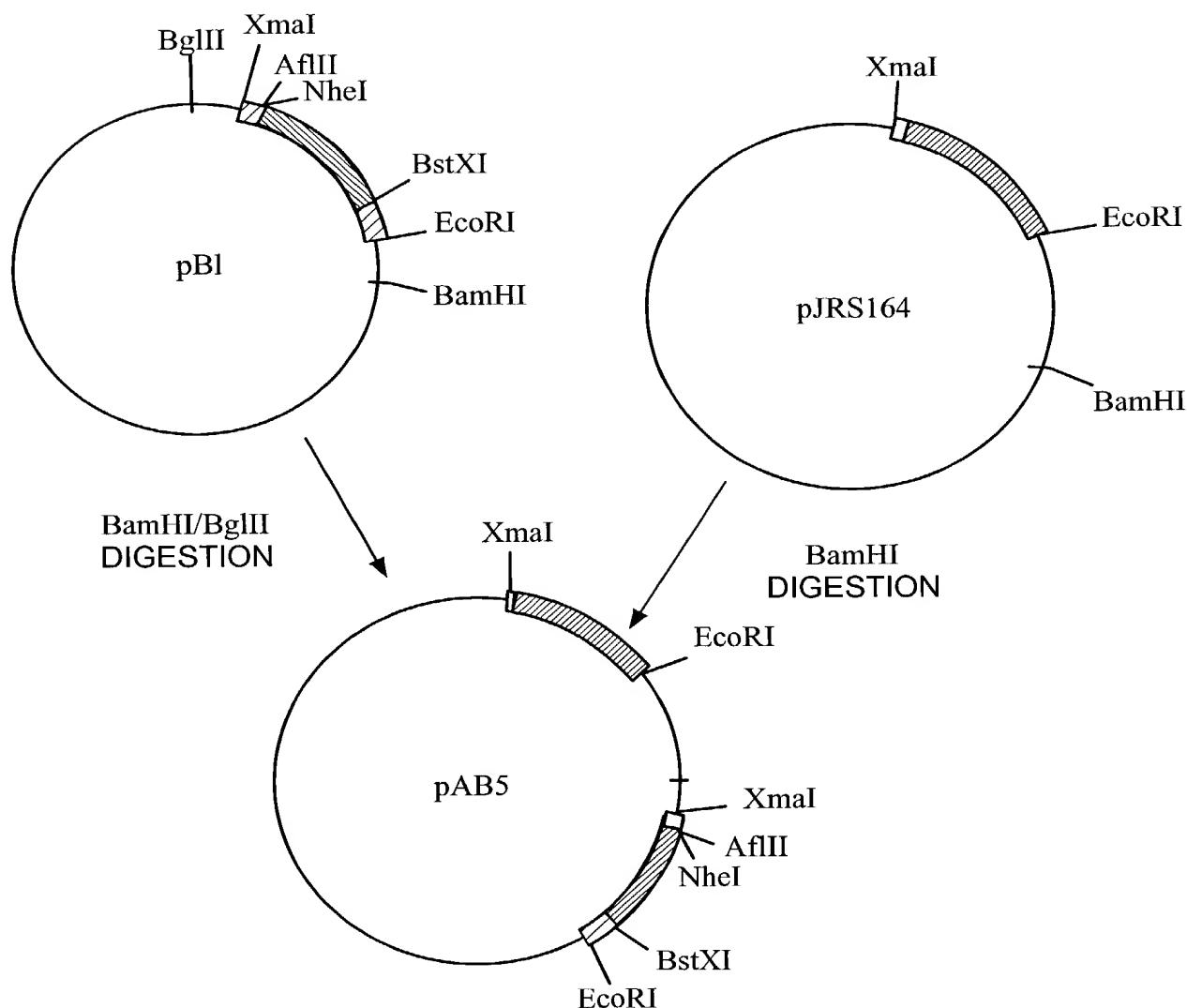


FIG. 19E

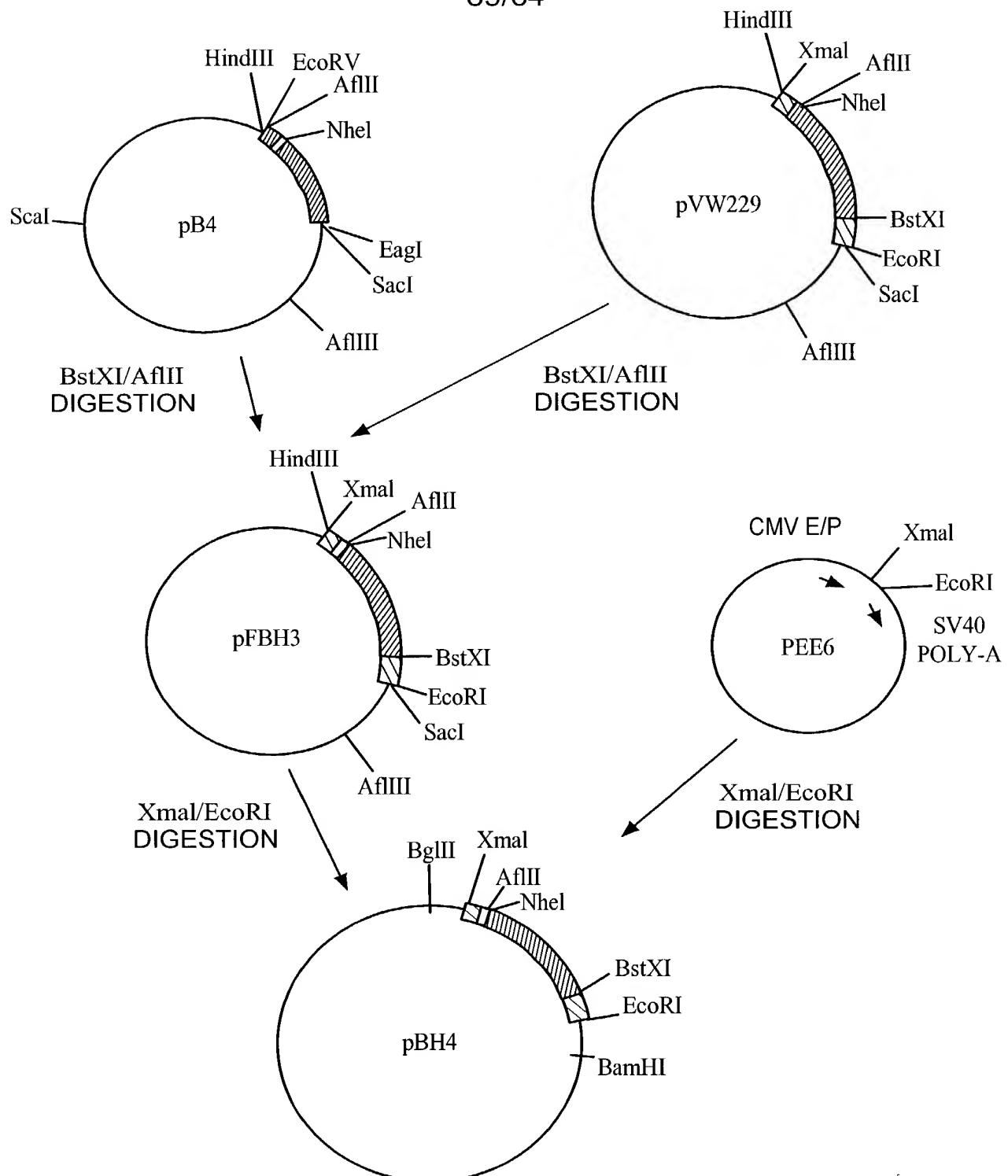


FIG. 19F

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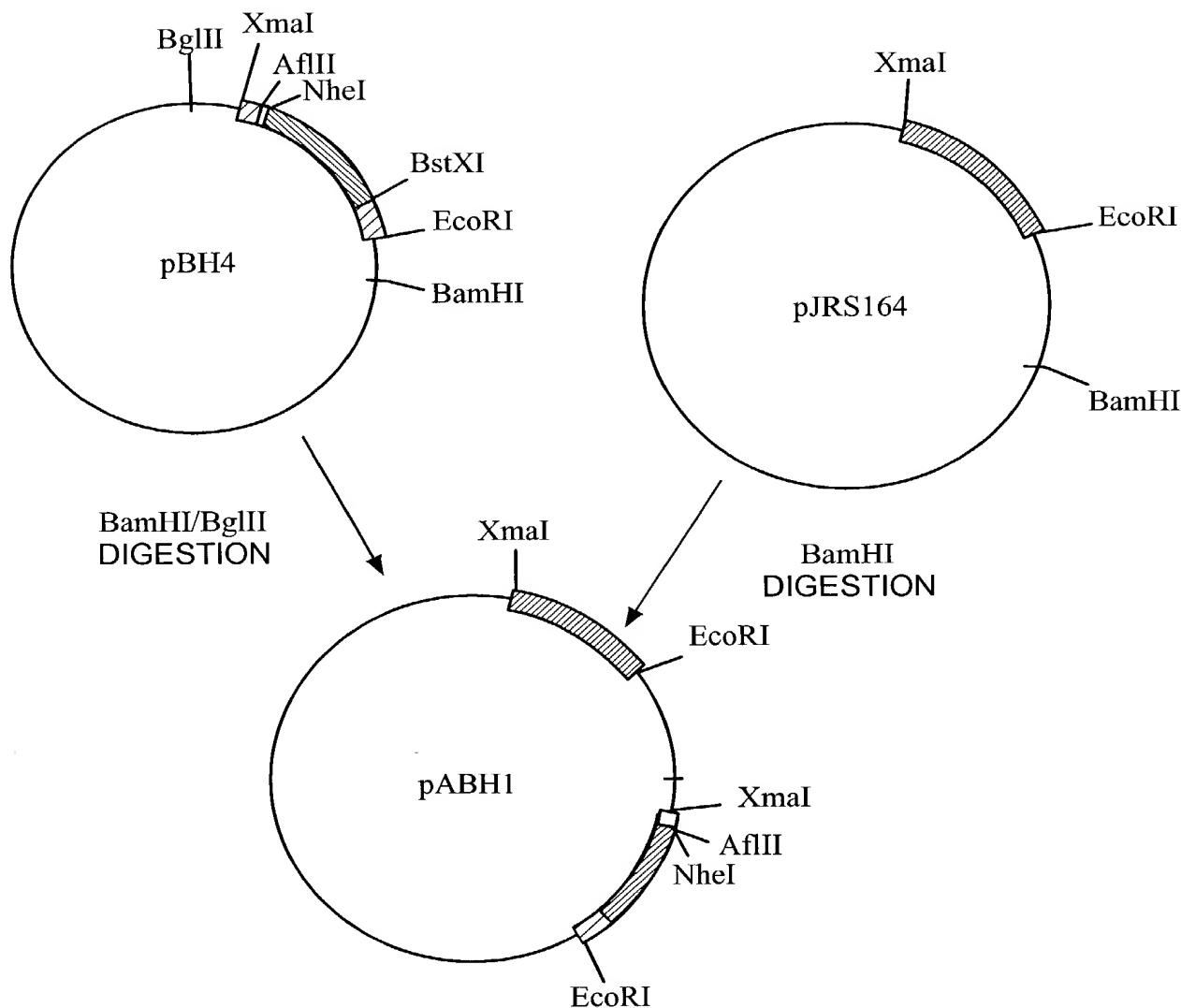


FIG. 19G

OLIGONUCLEOTIDES USED IN CLONING

OPR132

I-A^d β SIGNAL PEPTIDE FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR-
HindIII/XmaI SITES
5' -CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

I-A^d β SIGNAL PEPTIDE BACK PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- AfI III SITE
5' -CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

I-A^d β TRANSMEMBRANE FRONT PRIMER FOR CellTech VECTOR- BstXI SITES
5' -CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

I-A^d β TRANSMEMBRANE BACK PRIMER FOR CellTech VECTOR- SstI, EcoRI SITES
5' -CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'

OPR136

I-A^d α SIGNAL PEPTIDE FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR-
HindIII/XmaI SITES
5' -CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

I-A^d α TRANSMEMBRANE PRIMER FOR CellTech VECTOR- SstI/EcoRI SITES
5' -CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'

B7-1-2F

MURINE B7-1 FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- NotI SITES
5' -CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT
C-3'

B7-1-2B

MURINE B7-1 BACK PRIMER FOR CellTech VECTOR- NotI SITE
5' -CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

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NSO/ClassII/OVA CLONES STIMULATE IL-2
PRODUCTION FROM DO11.10

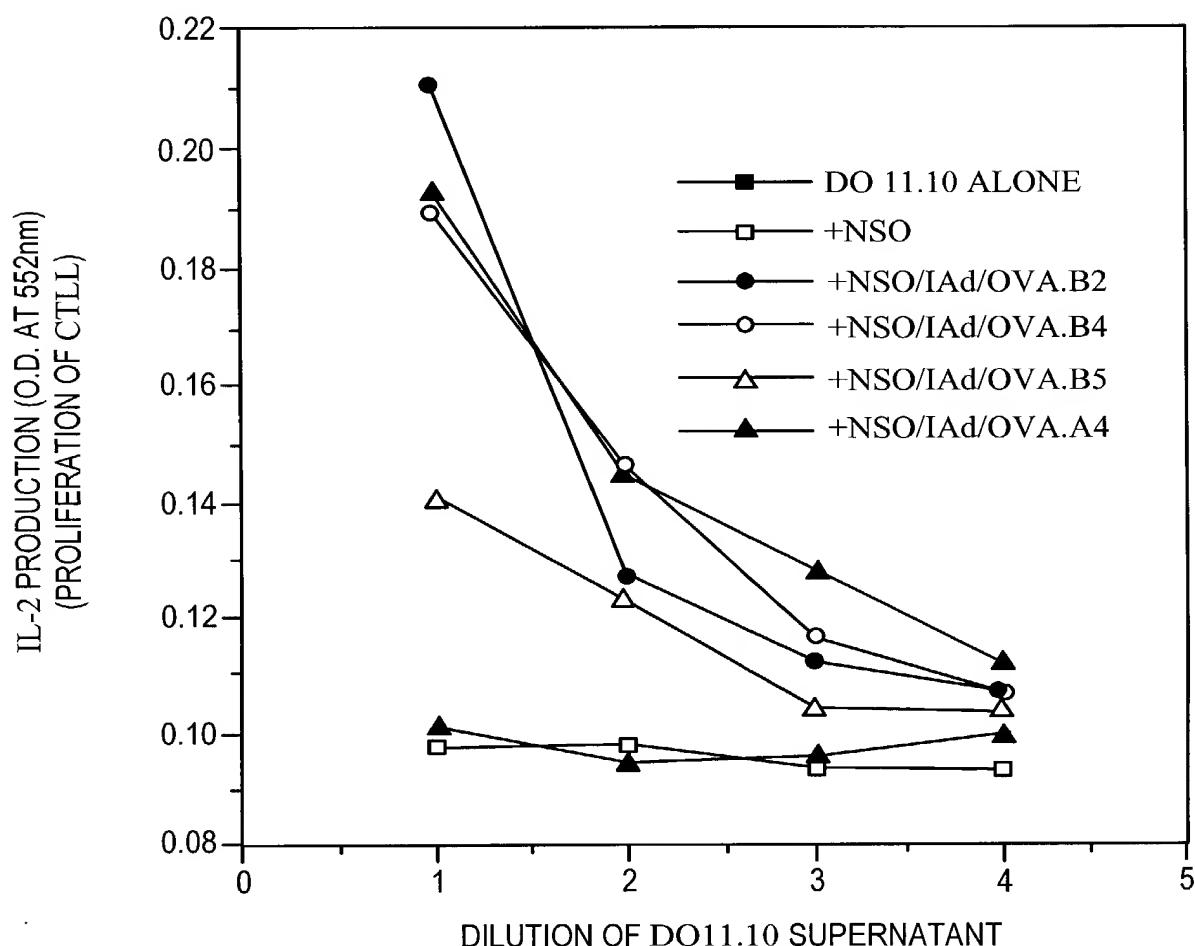


FIG. 21

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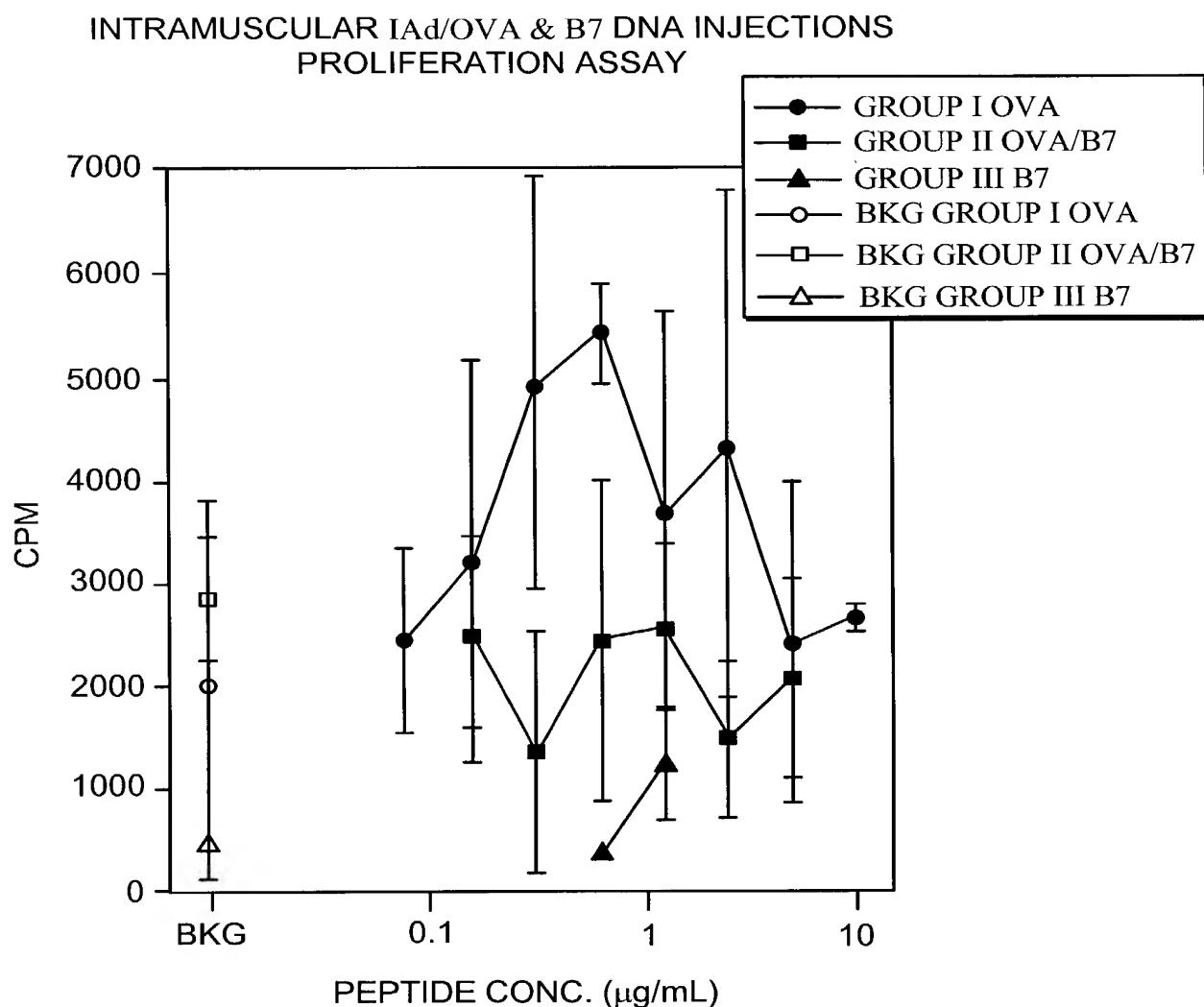


FIG. 22

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INTRADERMAL IAd/OVA & IAd/HEL DNA INJECTIONS
PROLIFERATION ASSAY
4, 7 & 14 DAYS POST INJECTION

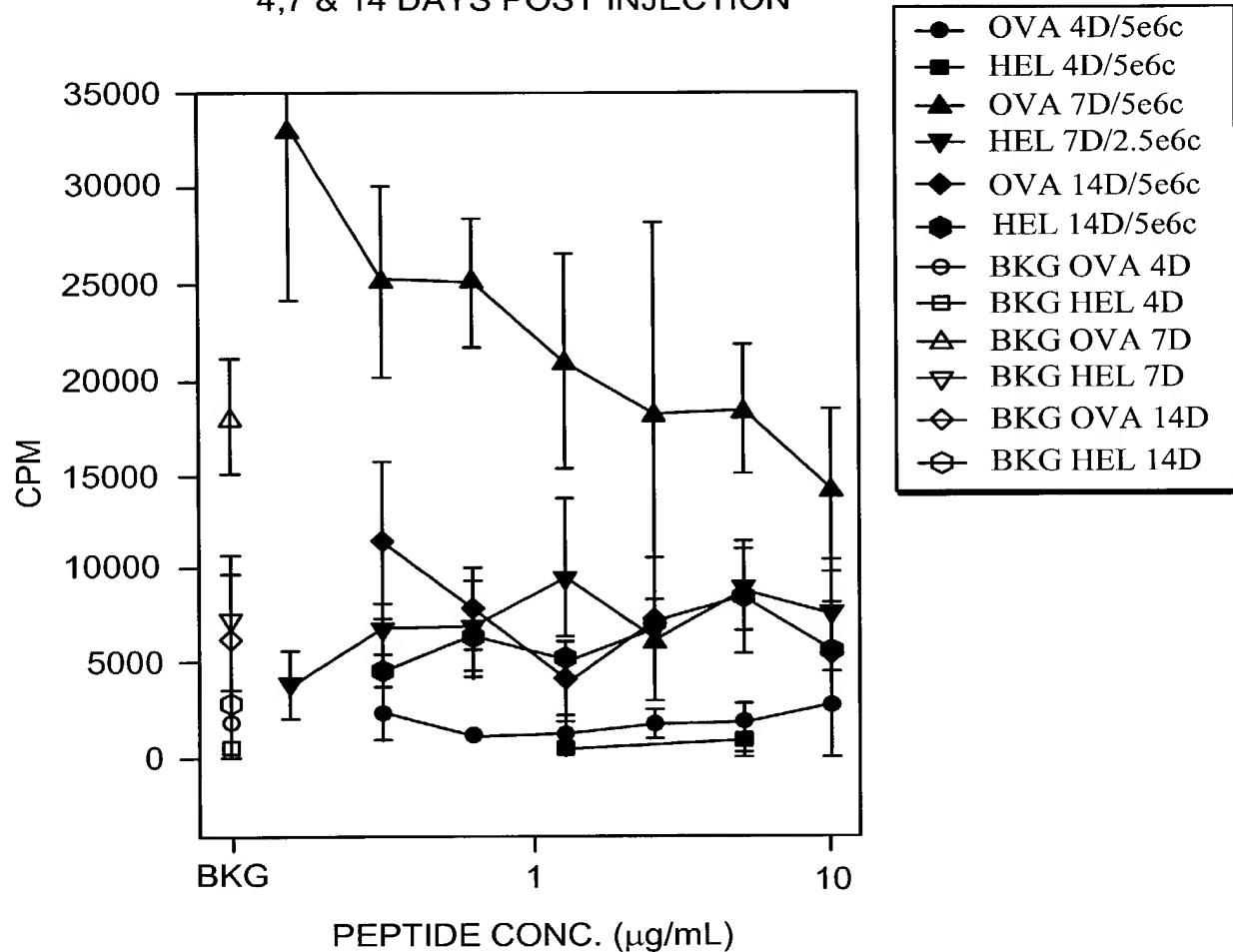
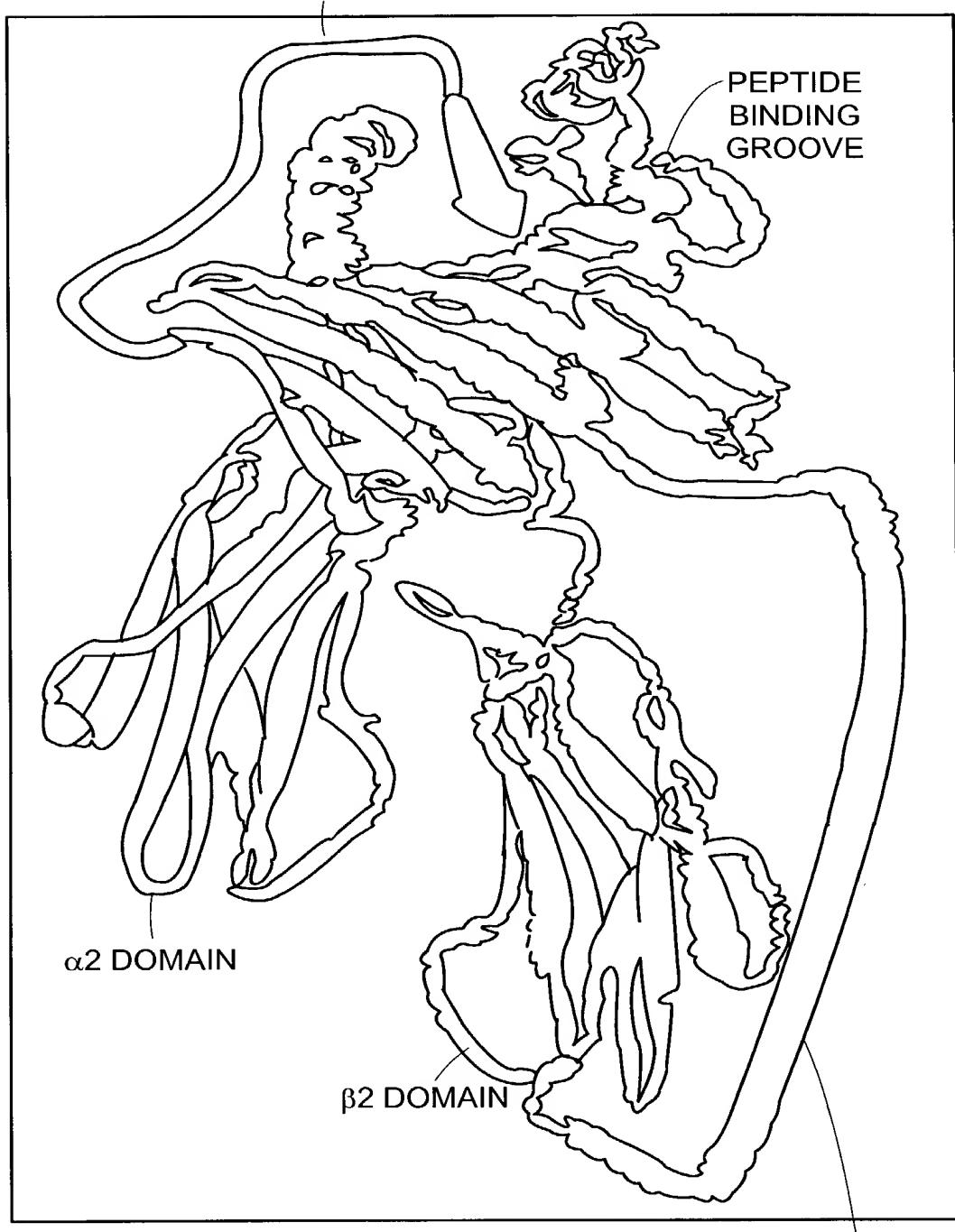


FIG. 23

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LINKER SEQUENCE LINKED
TO PRESENTING PEPTIDE



SINGLE CHAIN
LINKER SEQUENCE

FIG. 24

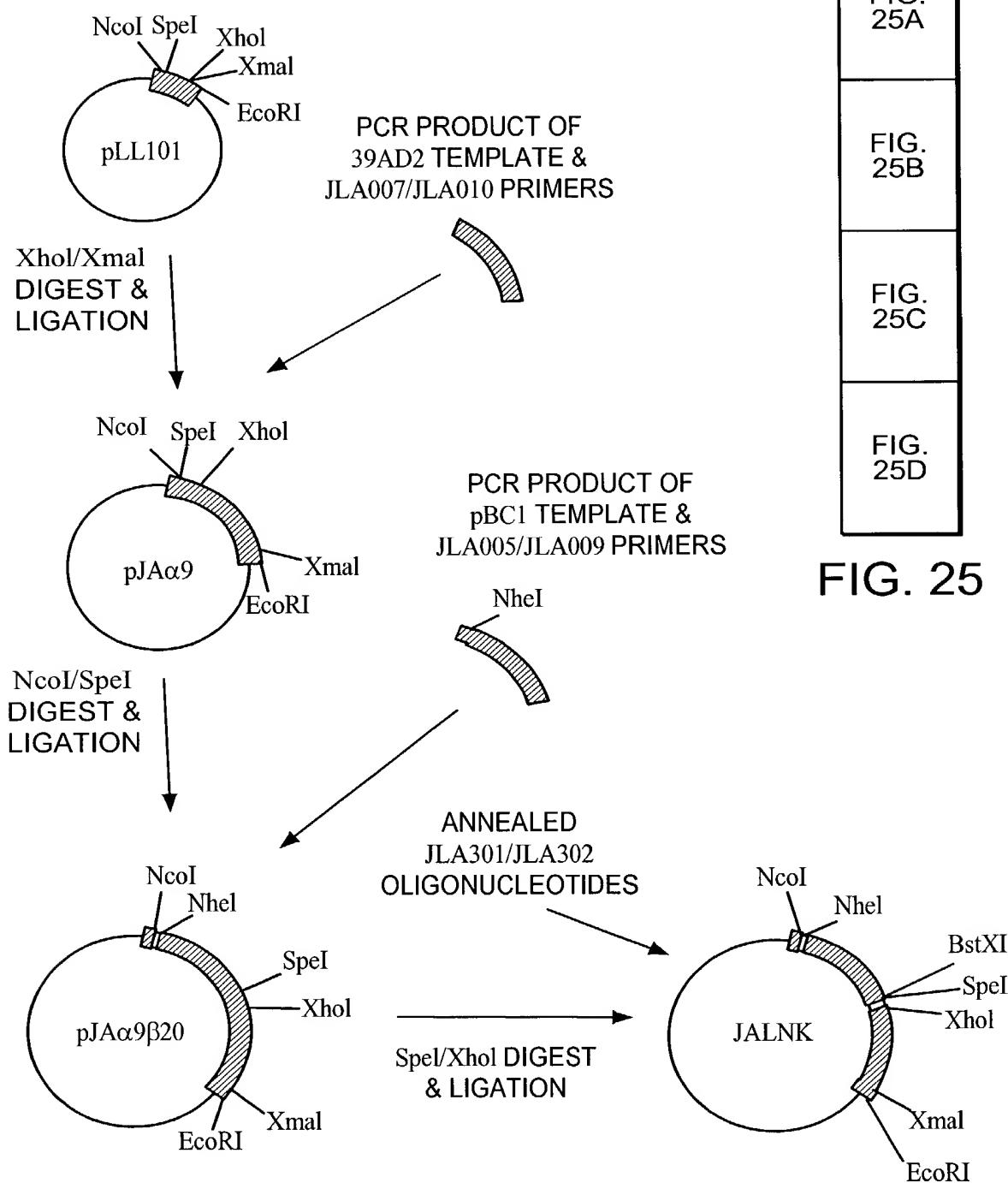
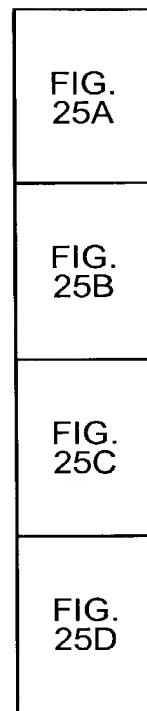


FIG. 25A

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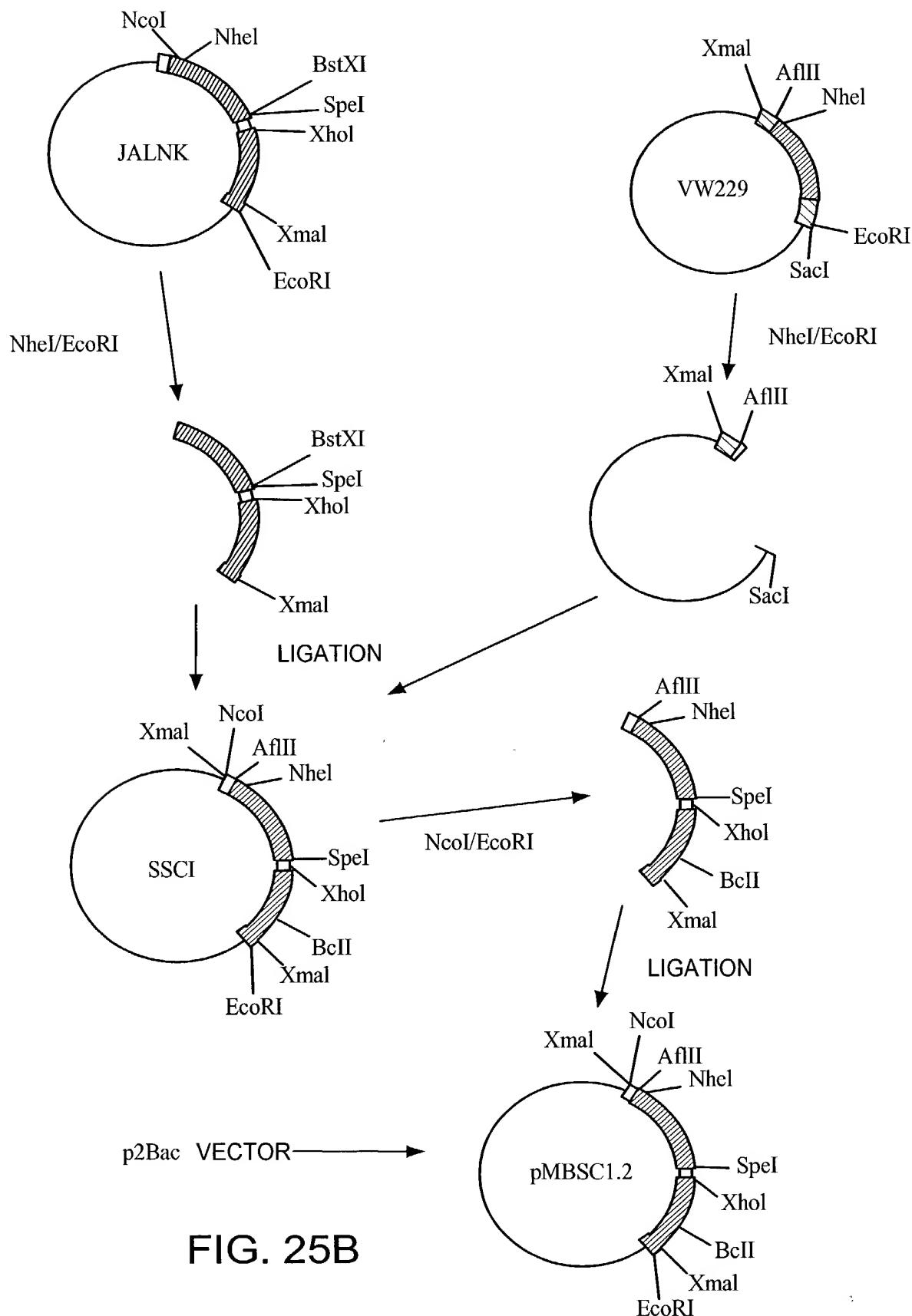


FIG. 25B

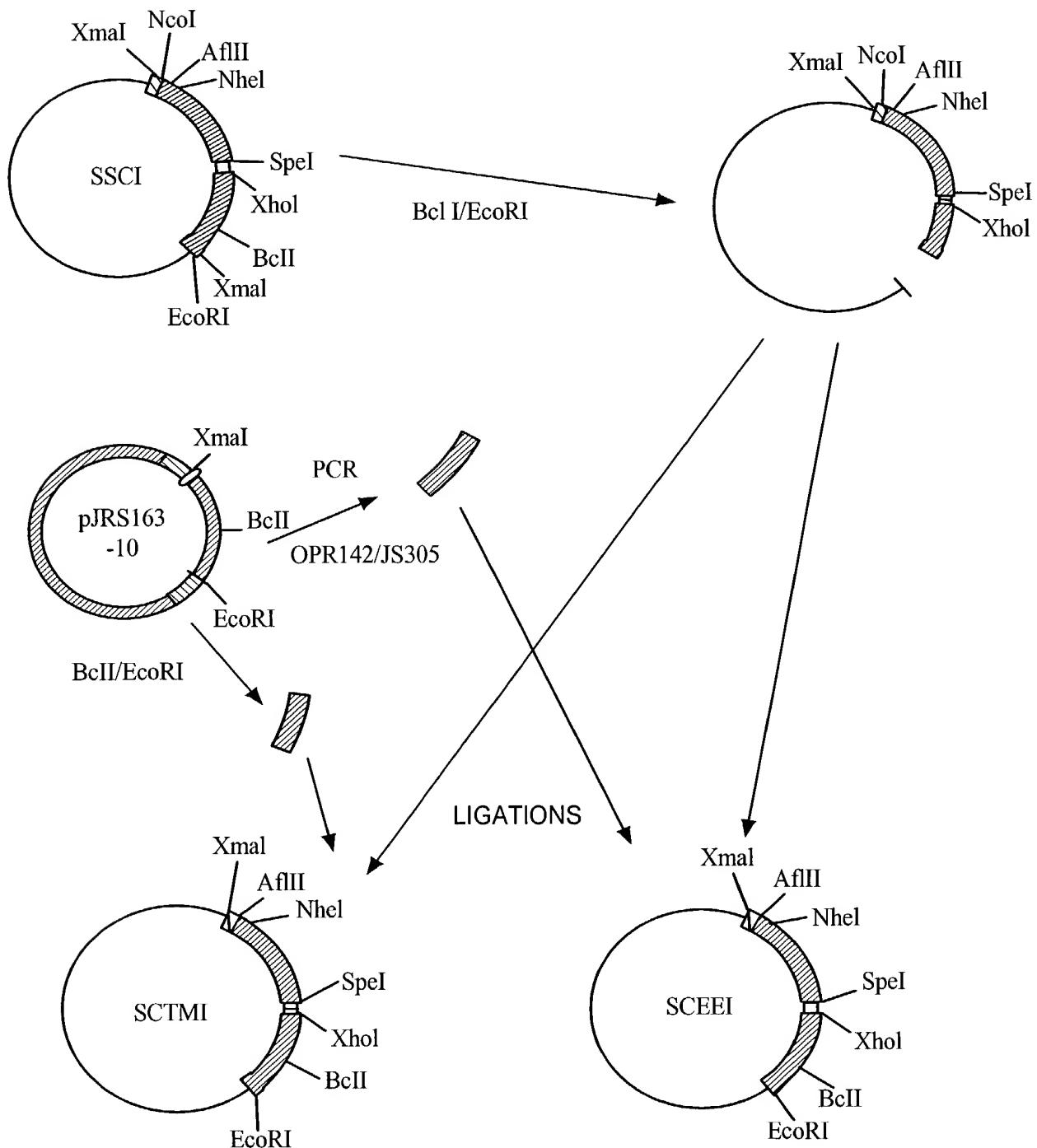


FIG. 25C

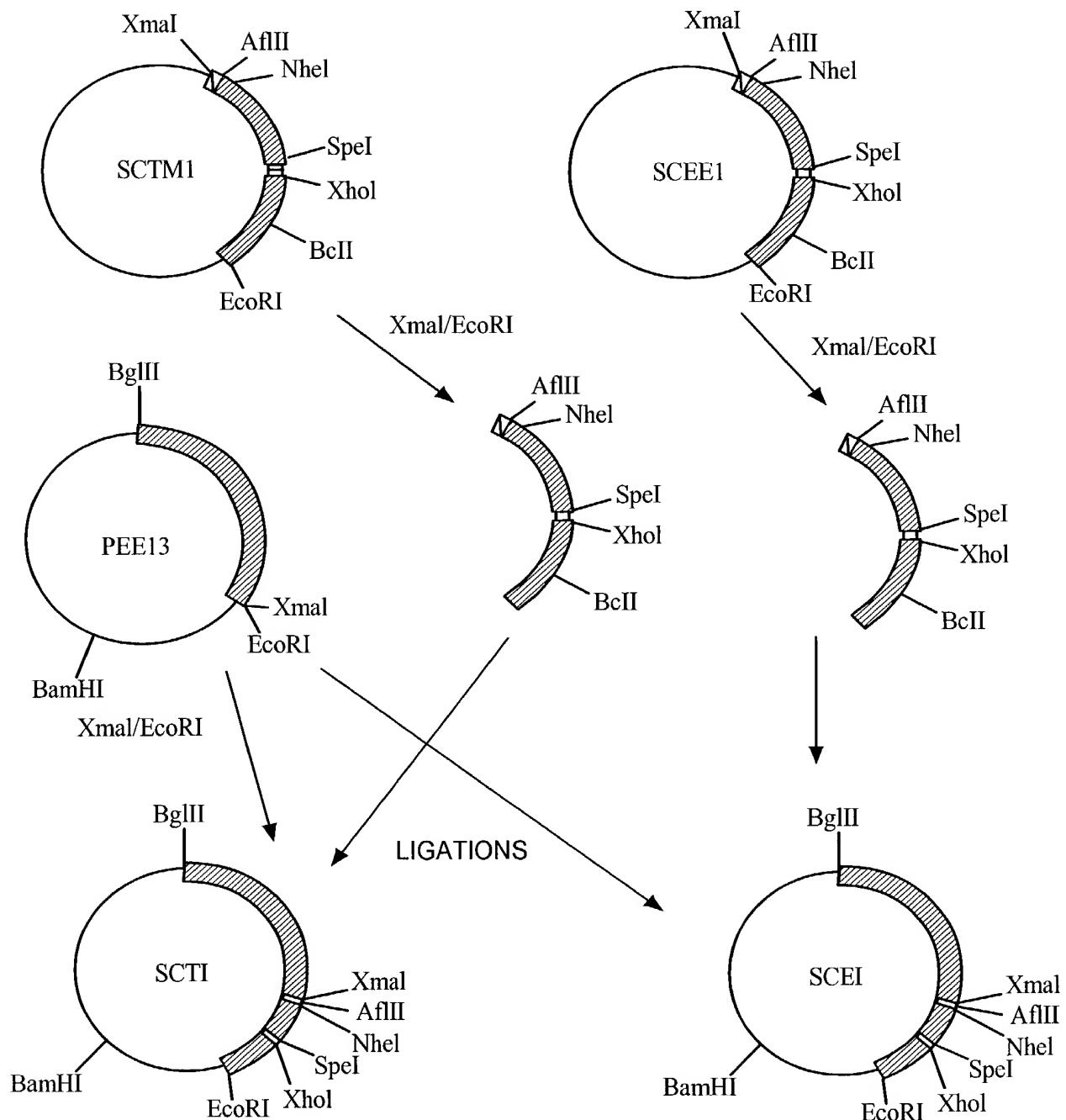


FIG. 25D

Title: MHC Complexes And Uses Thereof
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JLA-005

5' - CCCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC - 3'

JLA-007

5' - CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC - 3'

JLA-009

5' - CCCCCCACTAGTCCACTCCACAGTGATGGGCT - 3'

JLA-010

5' - CCCCCCCCCGGGACCAGTGTTCAGAACCGGCTCCTC - 3'

JLA-301

5' - TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGA-
 ACCACCACCGCCGCTGCCACCGCCACCA - 3'

JLA-302

5' - CTAGTGGTGGCGGTGGCAGCGCGGTGGTGGTCCGG-
 TGGCGGCGGTTCTGGCGGTGGCGGTTCC - 3'

OPR-142

5' - CTTGGGAATCTGACTAAGAGG - 3'

JS-305

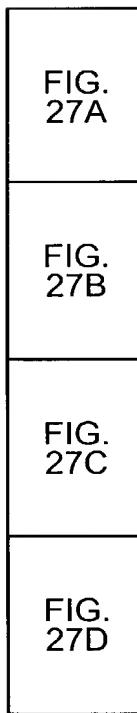
5' - CAGGTCGAATTCTCATTCCATCGGCATGTACTCTTCTT-
 CCTCCCAGTGTTCAGAACCGG - 3'

FIG. 26

FIG. 27

FIG. 27A

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10	20	30	40	50
* CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG	* GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG AGT CGA CGA CAC CAC	* M A L Q I P S L L L S A A V V>	* <----- I-Ad β CHAIN LEADER ----->	* -----
60	70	80	90	
* GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT	* CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA	* V L M V L S S P R T L S I S Q A>	* ><-----	
100	110	120	130	140
* GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA	* CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT	* V H A A H A E I N E A G R A S G>	* ><-----	
----- OVA 323-339 -----><-----				
150	160	170	180	190
* GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC	* CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG	* G G G S G G G N S E R H F V V>	* -- 10 AMINO ACID LINKER --><-----	* I-Ad β -1 DOMAIN ----->
200	210	220	230	240
* CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG	* GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC	* Q F K G E C Y Y T N G T Q R I R>	* -----	
250	260	270	280	290
* CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC	* GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG	* L V T R Y I Y N R E E Y V R Y D>	* -----	
300	310	320	330	
* AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC	* TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG	* S D V G E Y R A V T E L G R P D>	* -----	
340	350	360	370	380
* GCC GAG TAC TGG AAC AGC CAG CCC GAG ATC CTG GAG CGA ACG CGG GCC	* CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG	* A E Y W N S Q P E I L E R T R A>	* -----	

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FIG. 27B

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390	400	410	420	430											
*	*	*	*	*											
GAG	GTG	GAC	ACG	GCG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	CCG	GAG	ACC	AGC
CTC	CAC	CTG	TGC	CGC	ACG	TCT	GTG	TTG	ATG	CTC	CCC	GGC	CTC	TGG	TCG
E	V	D	T	A	C	R	H	N	Y	E	G	P	E	T	S>

440	450	460	470	480											
*	*	*	*	*											
ACC	TCC	CTG	CGG	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC	CTG	TCC
TGG	AGG	GAC	GCC	GCC	GAA	CTT	GTC	GGG	TTA	CAG	CGG	TAG	AGG	GAC	AGG
T	S	L	R	R	L	E	Q	P	N	V	A	I	S	L	S>
--- I-Ad β -1 DOMAIN -----><----- I-Ad β -2 DOMAIN -----															

490	500	510	520	530											
*	*	*	*	*											
AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG	GTG	ACA
TCC	TGT	CTG	CGG	GAG	TTG	GTG	GTG	TTG	TGA	GAC	CAG	ACA	AGC	CAC	TGT
R	T	E	A	L	N	H	H	N	T	L	V	C	S	V	T>

540	550	560	570												
*	*	*	*												
GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT	GGC	CAG
CTA	AAG	ATG	GGT	CGG	TTC	TAG	TTT	CAC	GCG	ACC	AAG	TCC	TTA	CCG	GTC
D	F	Y	P	A	K	I	K	V	R	W	F	R	N	G	Q>

580	590	600	610	620											
*	*	*	*	*											
GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	GAC
CTC	CTC	TGT	CAC	CCC	CAG	AGT	AGG	TGT	GTC	GAA	TAA	TCC	TTA	CCC	CTG
E	E	T	V	G	V	S	S	T	Q	L	I	R	N	G	D>

630	640	650	660	670											
*	*	*	*	*											
TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	GGA
ACC	TGG	AAG	GTC	CAG	GAC	CAG	TAC	GAC	CTC	TAC	TGG	GGA	GTA	GTC	CCT
W	T	F	Q	V	L	V	M	L	E	N	T	P	H	Q	G>

680	690	700	710	720											
*	*	*	*	*											
GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	ATC
CTC	CAG	ATG	TGG	ACG	GTA	CAC	CTC	GTA	GGG	TCG	GAC	TTC	TCG	GGG	TAG
E	V	V	T	C	H	V	E	H	P	S	L	A	S	P	I>

I-Ad β -2 DOMAIN -----															
730	740	750	760	770											
*	*	*	*	*											
ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGC	AGC	GGC	GGT	GGT	GGT	TCC	
TCA	CAC	CTC	ACC	TGA	TCA	CCA	CCG	CCA	CCG	TCG	CCG	CCA	CCA	CCA	AGG
T	V	E	W	T	S	G	G	G	S	G	G	G	G	S>	

24 AMINO ACID LINKER -----														
----------------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--

FIG. 27C

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780	790	800	810	
* GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCC ACT GAA GAC GAC ATT	* CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA	* G G G G S G G G S S S E D D I>	* ><	
----- I-Ad α -1 DOMAIN -----				
820	830	840	850	860
* GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT	* CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA	* E A D H V G F Y G T T V Y Q S P>	* ><	
----- I-Ad α -1 DOMAIN -----				
870	880	890	900	910
* GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTC TTC	* CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG	* G D I G Q Y T H E F D G D E L F>	* ><	
----- I-Ad α -1 DOMAIN -----				
920	930	940	950	960
* TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT	* ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA	* Y V D L D K K T V W R L P E F>	* ><	
----- I-Ad α -1 DOMAIN -----				
970	980	990	1000	1010
* GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT	* CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA	* G Q L I L F E P Q G G L Q N I A>	* ><	
----- I-Ad α -1 DOMAIN -----				
1020	1030	1040	1050	
* GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC	* CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG	* A E K H N L G I L T K R S N F T>	* ><	
----- I-Ad α -1 DOMAIN -----				
1060	1070	1080	1090	1100
* CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT	* GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA	* P A T N E A P Q A T V F P K S P>	* ><	
----- I-Ad α -2 DOMAIN -----				
1110	1120	1130	1140	1150
* GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC	* CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG	* V L L G Q P N T L I C F V D N T>	* ><	
----- I-Ad α -2 DOMAIN -----				

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1160	1170	1180	1190	1200
*	*	*	*	*
TTC CCA GCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC				
AAG GGT GGA CAC TAG TTG TAG TGT ACG GAG TCT TTA TCG TTC AGT CAG				
F P P V I N I T W L R N S K S V>				
<hr/>				
1210	1220	1230	1240	1250
*	*	*	*	*
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC				
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG				
T D G V Y E T S F L V N R D H S>				
<hr/>				
1260	1270	1280	1290	
*	*	*	*	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT				
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA				
F H K L S Y L T F I P S D D D I>				
<hr/>				
1300	1310	1320	1330	1340
*	*	*	*	*
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA				
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT				
Y D C K V E H W G L E E P V L K>				
<hr/> I-Ad α -2 DOMAIN <hr/>				
1350	1360	1370	1380	
*	*	*	*	
CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAC TAG				
GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTG ATC				
H W S R A S H H H H H H * >				
<hr/> >< 6 X HIS TAG -->				

FIG. 27D

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Title: MHC Complexes And Uses Thereof
Inventor(s): W. G. W., et al.

Inventor(s): Hing C. Wong, et al.

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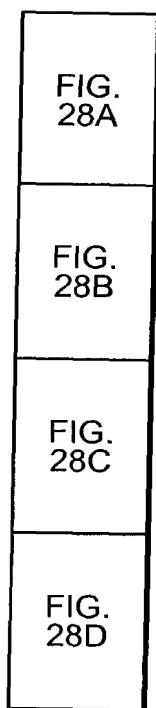


FIG. 28

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FIG. 28A

10 * 20 * 30 * 40 * 50 *

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TGA GCT GCT GTG GTG
 GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG AGT CGA CGA CAC CAC
 M A L Q I P S L L L S A A V V>
 <----- I-Ad β CHAIN LEADER ----->

60 * 70 * 80 * 90 *

GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
 CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V L M V L S S P R T L S I S Q A>
 -----><-----

100 * 110 * 120 * 130 * 140 *

GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
 CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V H A A H A E I N E A G R A S G>
 -----><----- OVA 323-339 -----><-----

150 * 160 * 170 * 180 * 190 *

GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
 CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G G G S G G G N S E R H F V V>
 ---10 AMINO ACID LINKER--><----- I-Ad β -1 DOMAIN ----->

200 * 210 * 220 * 230 * 240 *

CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
 GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
 Q F L G E C Y Y T N G T Q R I R>

250 * 260 * 270 * 280 * 290 *

CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
 GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L V T R Y I Y N R E E Y V R Y D>

300 * 310 * 320 * 330 *

AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S D V G E Y R A V T E L G R P D>

340 * 350 * 360 * 370 * 380 *

GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A E Y W N S Q P E I L E R T R A>

FIG. 28B

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390	400	410	420	430
*	*	*	*	*
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG E V D T A C R H N Y E G P E T S>				
<hr/>				
440	450	460	470	480
*	*	*	*	*
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG T S L R R L E Q P N V A I S L S> --- I-Ad β -1 DOMAIN ----->----- I-Ad β -2 DOMAIN -----				
<hr/>				
490	500	510	520	530
*	*	*	*	*
AGG ACA GAG GCC CTC AAG CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT R T E A L N H H N T L V C S V T>				
<hr/>				
540	550	560	570	
*	*	*	*	
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC D F Y P A K I K V R W F R N G Q>				
<hr/>				
580	590	600	610	620
*	*	*	*	*
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG E E T V G V S S T Q L I R N G D>				
<hr/>				
630	640	650	660	670
*	*	*	*	*
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT W T F Q V L V M L E M T P H Q G>				
<hr/>				
680	690	700	710	720
*	*	*	*	*
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG E V Y T C H V E H P S L K S P I> ----- I-Ad β -2 DOMAIN -----				
<hr/>				
730	740	750	760	770
*	*	*	*	*
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT TCC TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG T V E W T S G G G G S G G G G G S> ----- 24 AMINO ACID LINKER -----				

Title: MHC Complexes And Uses Thereof

Inventor(s): Hing C. Wong, et al.

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FIG. 28C

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780	790	800	810	
*	*	*	*	
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT	CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA	G G G G S G G G S S S E D D I>	><	
820	830	840	850	860
*	*	*	*	*
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT	CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA	E A D H V G F Y G T T V Y Q S P>	I-Ad α -1 DOMAIN	
870	880	890	900	910
*	*	*	*	*
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC	CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG	G D I G Q Y T H E F D G D E L F>		
920	930	940	950	960
*	*	*	*	*
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT	ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA	Y V D L D K K K T V W R L P E F>		
970	980	990	1000	1010
*	*	*	*	*
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT	CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA	G Q L I L F E P Q G G L Q N I A>		
1020	1030	1040	1050	
*	*	*	*	
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC	CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG	A E K H N L G I L T K R S N F T>	I-Ad α -1 DOMAIN	
1060	1070	1080	1090	1100
*	*	*	*	*
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT	GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA	P A T N E A P Q A T V F P K S P>	><	I-Ad α -2 DOMAIN
1110	1120	1130	1140	1150
*	*	*	*	*
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC	CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG	V L L G Q P N T L I C F V D N I>		

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1160 * TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTG AAG GGT GGA CAC TAG TTG TAG TGT ACG GAG TCT TTA TCG TTC AGT CAG F P P V I N I T W L R N S K S V>	1170 * -----	1180 * -----	1190 * -----	1200 * -----
1210 * ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG T D G V Y E T S F L V N R D H S>	1220 * -----	1230 * -----	1240 * -----	1250 * -----
1260 * TTC CAC AAG CTG TCT TAT CTC ACG TTC ATC CCT TCT GAT GAT GAC ATT AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA F H K L S Y L T F I P S D D D I>	1270 * -----	1280 * -----	1290 * -----	-----
1300 * TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGG CAA GAC TTT Y D C K V E H W G L E E P V L X>	1310 * -----	1320 * -----	1330 * -----	1340 * ----- I-Ad α -2 DOMAIN -----
1350 * CAC TCG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA H N E P E I P A P M S E L T E T>	1360 * -----><----- I-Ad α -TM DOMAIN -----	1370 * -----	1380 * -----	1390 * -----
1400 * GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC V V C A L G L S V G L V G I V V>	1410 * -----	1420 * -----	1430 * -----	1440 * -----
1450 * GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA CCG TGG TAG AAG TAG TAA GTT CCG GAG GCT AGT CCA CCG TGG AGG TCT G T I F I I Q G L R S G G T S R>	1460 * -----	1470 * -----	1480 * -----	1490 * -----
1500 * CAC CCA GGG CCT TTA TGA GTG GGT CCC GGA AAT ACT H P G P L *> -- I-Ad α -TM DOMAIN ->	-----	-----	-----	-----

FIG. 28D

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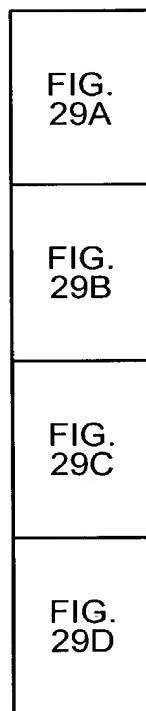


FIG. 29

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FIG. 29A

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10 * 20 * 30 * 40 * 50 *

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
 GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
 M A L Q I P S L L L S A A V V>
 <----- I-Ad β CHAIN LEADER ----->

60 * 70 * 80 * 90 *

G TG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
 CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V L M V L S S P R T L S I S Q A>
 -----><-----

100 * 110 * 120 * 130 * 140 *

GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
 CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CGA GCA CGA TCG CCT
 V H A A H A E I N E A G R A S G>
 ----- OVA 323-339 -----><-----

150 * 160 * 170 * 180 * 190 *

GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
 CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G G G S G G G N S E R H F V V>
 ---10 AMINO ACID LINKER--><----- I-Ad β -1 DOMAIN ----->

200 * 210 * 220 * 230 * 240 *

CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
 GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
 Q F K G E C Y Y T N G T Q R I R>

250 * 260 * 270 * 280 * 290 *

CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
 GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L V T R Y I Y N R E E Y V R Y D>

300 * 310 * 320 * 330 *

AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S D V G E Y R A V T E L G R P D>

340 * 350 * 360 * 370 * 380 *

GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A E Y W N S Q P E I L E R T R A>

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FIG. 29B

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390 * 400 * 410 * 420 * 430 *

GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E V D T A C R H N Y E G P E T S >

440 * 450 * 460 * 470 * 480 *

ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T S L R R L E Q P N V A I S L S >

----- I-Ad β -1 DOMAIN -----><----- I-Ad β -2 DOMAIN -----

490 * 500 * 510 * 520 * 530 *

AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R T E A L N H H N T L V C S V T >

540 * 550 * 560 * 570 *

GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D F Y P A K I K V R W F R N G Q >

580 * 590 * 600 * 610 * 620 *

GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E E T V G V S S T Q L I R N G D >

630 * 640 * 650 * 660 * 670 *

TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
 ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W T F Q V L V M L F M T P H Q G >

680 * 690 * 700 * 710 * 720 *

GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E V Y T C H V E H P S L K S P I >

----- I-Ad β -2 DOMAIN -----

730 * 740 * 750 * 760 * 770 *

ACT GTG GAG TGG ACT AGT GGT GGG GGT GGC AGC GGC GGT GGT TCC
 TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T V E W T S G G G G S G G G G S >

><----- 24 AMINO ACID LINKER ----->

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FIG. 29C

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780 * GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCC AGT GAA GAC GAC ATT CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA G G G G S G G G S S S E D D I>	790 * -----><-----	800 * -----><-----	810 * -----><-----	
<hr/>				
820 * GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT CTC CCG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA E A C H V G F Y G T T V Y Q S P>	830 * -----><----- I-Ad α -1 DOMAIN	840 * -----><-----	850 * -----><-----	860 * -----><-----
<hr/>				
870 * GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG G D I G Q Y T H E F D G D E L F>	880 * -----><-----	890 * -----><-----	900 * -----><-----	910 * -----><-----
<hr/>				
920 * TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA Y V D L D K K T V W R L P E F>	930 * -----><-----	940 * -----><-----	950 * -----><-----	960 * -----><-----
<hr/>				
970 * GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GSA CTG CAA AAC ATA GCT CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA G Q L I L F E P Q G G L Q N I A>	980 * -----><-----	990 * -----><-----	1000 * -----><-----	1010 * -----><-----
<hr/>				
1020 * GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG A E K H N L G I L T K R S N F T>	1030 * -----><----- I-Ad α -1 DOMAIN	1040 * -----><-----	1050 * -----><-----	
<hr/>				
1060 * CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GGT CGA TGG TTA CTC CGA CGA GTT CGC TGA CAC AAG GGG TTC AGG GGA P A T N E A P Q A T V F P K S P>	1070 * -----><----- I-Ad α -2 DOMAIN	1080 * -----><-----	1090 * -----><-----	1100 * -----><-----
<hr/>				
1110 * GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG V L L G Q P N T L I C F V D N I>	1120 * -----><-----	1130 * -----><-----	1140 * -----><-----	1150 * -----><-----
<hr/>				

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1160

*
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC

1170

*
AAG GGT GGA CAC TAG TTG TAG TGT ACS GAG TCT TTA TCG TTC AGT CAG

F P P V I N I T W L R N S K S V>

1180

*

1190

*

1200

*

1210

*
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC

1220

*
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG

T D G V Y E T S F L V N R D H S>

1230

*

1240

*

1250

*

1260

*
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT

1270

*
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA

F H K L S Y L T F I P S D D D I>

1280

*

1290

*

1300

*
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA

1310

*
ATA CTG ACG TTC CAC CTC GTG ACC CSS GAC CTC CTC GGC CAA GAC TTT

1320

*
Y D C K V E H W G L E E P V L K>

1330

*

1340

*
-----I-Ad α -2 DOMAIN -----

1350

*
CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA

1360

*
GTG ACC CTC CTT CTC ATG TAC GGC TAC CTT ACT

1370

*
H W E E E E Y M P M E *>

1380

*

><----- EE TAG ----->

FIG. 29D